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From:

Walicka, Malgorzata

Sent:

Saturday, October 29, 2005 10:56 AM

To:

STIC-Biotech/ChemLib

Please search SEQ ID NO:1 and 16 in 09/774,954. Please use also pending data.

Thank you.

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Alexandria, VA 22313
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Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA#
S/L:
Oligomer:
Encode/Transl:
Structure #:
Inventor:
Litigation:

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM
WWW/Internet:
Other (Specify):

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GenCore version (c) 1993 - 2005 using sw model 2005, 23:53:44	ct score: 15.74-954-1 ct score: 15.14-7.74-954-1 nce: 1 ATGCCGCGGGCTCCTGGGA ng table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 hed: 4708233 seqs, 24227607955 resi number of hits satisfying chosen parametum DB seq length: 0 um DB seq length: 0 processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1: gb_ba:* 2: gb_htg:* 3: gb_in:* 4: gb_om:* 5: gb_ov:* 6: gb_pat:* 7: gb_ph:* 8: gb_pl:* 9: gb_pl:* 10: gb_ro:* 11: gb_ro:* 12: gb_pr:* 12: gb_yr:* 13: gb_vi:* 14: gb_vi:* 14: gb_vi:* 14: gb_vi:* 14: gb_vi:* 15: gb_vi:* 16: gb_vi:* 17: gb_vi:* 18: gb_vi:* 19: gb_vi:* 19: gb_vi:* 10: gb_vi:* 10: gb_vi:* 11: gb_vi:* 12: gb_vi:* 13: gb_vi:* 14: gb_vi:* 14: gb_vi:* 15: gb_vi:* 16: gb_vi:* 17: gb_vi:* 18: gb_vi:* 18: gb_vi:* 19: gb_vi:* 19: gb_vi:* 19: gb_vi:* 10: gb_vi:* 10: gb_vi:* 10: gb_vi:* 10: gb_vi:* 11: gb_vi:* 12: gb_vi:* 13: gb_vi:* 14: gb_vi:* 15: gb_vi:* 16: gb_vi:* 17: gb_vi:* 17: gb_vi:* 18: gb_vi:* 18: gb_vi:* 19: gb_vi:* 19: gb_vi:* 19: gb_vi:* 19: gb_vi:* 10:	Pegult Score Match Length DB ID 1 1514 100.0 1514 6 AR163451 2 1512.4 99.9 5249 9 AF375884 5 1510.8 99.9 5249 9 AF375884 5 1510.8 99.9 5266 6 AX780153 7 1507.6 99.6 4560 9 HSM803330 8 1447.4 95.6 5009 6 BD103191 10 1163.4 76.8 1300 6 AR163453 11 1163.4 76.8 1300 6 AR163453 11 1163.4 76.8 1300 6 AR163457 11 1163.4 76.8 1300 6 AR163457 11 1163.4 76.8 1300 6 BD103191 12 1100 72.7 1100 6 BD103199 13 1100 72.7 1100 6 BD103196 14 1096.4 72.8 1167 6 CQ77777 15 1086.8 72.8 1167 6 AX781500 16 916.2 60.5 1176 4 AX781503 17 908.2 60.0 1176 4 AX781503 18 901.6 59.6 1134 4 SSC567917

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/cell_type="myeloblast"
/tissue_type="brain"
/clone_lib="plathescriptII SK plus"
/note="This sequence was obtained by subcloning of the |
fragments derived from two cDNA clones (1 - 1066 was
derived from pf00933 and 1067 - 5189 was derived from
ha00267).
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larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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/gene="KIAA0180"
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa, Chordata; Catarrhini; Hominidae; Homo.

Eutheria; Dutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 4560)

Nambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

Direct Submission

L Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ)4510114) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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Homo sapiens mRNA; cDNA DKFZp45lJ114 (from clone DKFZp45lJ114).
AL832023
                                           CAGTCGGTCTACCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
                                                                                                            AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCTGAGGTCGAGTCGAACTTC
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                         CAGTCGGTCTACGTTGCTACTGATTCCGAGGTTATGTGCCCTGAGCTCCAACAGCTCTTC
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Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Bugas, M., Ells, R., Brors, B. and Mergenthaler, S. Novel Benetic markers for leukemias Patent: WO 03039443-A 2310 15-MAY-2003, Deutsches Krebsforschungszentrum (DE); Ludwig-Maximilian-Universitaet Muenchen (DE); PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, M. Location/Qualifiers
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                                                                                                                                                                                                                                Score 1509.8;
Pred. No. 0;
                                                                                                                              1. .5266
/organism="Homo sapiens"
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/db_xref="taxon;9606"
                                                                                                                                                                                                                                                                0; Mismatches
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larity 99.8%;
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Best Local Similarity
Matches 1511; Conserv
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                                                          CAGTCGGTCTACCTACCGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
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                                                                                        AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC
                                                                                                                                       CTCGGCCAAGCCGACTTTATTGGCAACTGTCTCCTTCACTGCCTTTGTGAAG
CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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Wang, Y. and Spellman, M. W.
Wolfucosyltransferase
Patent: US 6270987-A 8 07-AUG-2001;
Location/Qualifiers
1. 5009
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Sequence 8 from patent US 6270987.
AR163453 GI:16234058
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 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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                                              1. .4560

/mol Lyge=mnRNA.

/mol Lyge=mnRNA.

/db_xref="Rx2D:DKF2p451J114"

/db_xref="Rx2D:9606"

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/tissue type="human skeletal muscle"

/clone lib="451 (synonym: hlccl). Vector pSportl; host

DH108: ii.b="451 (synonym: hlccl). Vector pSportl; host

dev_stage="adult"
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Pred. No. 0;
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Best Local Similarity 99.7%;
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	RESULT 9 BD103191 BD103191	Query Match Best Local Similarity 99.9%; Pred. No. 0; Bact Local Sinilarity 99.9%; Pred. No. 0; Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 66 GAACCAGGCCGATCACTTTGGCCTCTTGGCATTTGCAAAGCGTAAACCGTACCTT 125
Query Match 95.6%; Score 1447.4; DB 6; Length 5009; Best Local Similarity 99.9%; Pred. No. 0; 1; Indels 0; Gaps 0; Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 0; Mismatches 1; Indels 0; Gaps 0; Qy 66 GAACCAGGCCATCACTTCTGGCTCTTGGCATTTGCAAAGCTGCTAAACCGTACTT 125 1 GAACCAGGCGATCACTTCTGGCTCTTTGGCATTTGCAAAGCTGCTACTT 185 Db 126 GGCTGTCCCTTCTGGATTGGTACCAGCATCACAAGCTCCTTTCACCAACTTCACTGT 120 09 127 GGCTGTCCTTCTGGATTCAAGCTGGACACTCCTTTCACCAACTTCACTGTT 120 09 128 GGCTGTCCCTTCGAATTCAAGCTGGACACCCTCCTTTCACCAACTTCACTGACTT 120 09 129 GGCTGTCCCTTCGAATTCAAGCTGGACCCCTCCAAGCTTACCAACTCCATTTCACTACTT 180 09 120 GGCTGTCCTTCAGAATTCAAGCTGGACCCCTCCAAGCTCCTTTCACCAACTCAACTTCAACTT 180 09 246 GGAGATTTCAAGGAGACCCCACCACACACAACACTCCCCCTCCAAGAACTGAAGCAATTACAAGAACTGAAGCAATTACAACAACTGAAGCAACTGAAGCAACTGAAGCAACTGAAGCAACTGAAGCAACTGAAGCAACTGAAGCAACTGAAGCAACAACAACAACAACAACAACAACAACAACAACAA	99 486 GGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCTCCCGTCTTAGAGAACA 48.6 90 421 [1026 GCGGGACCTCCAGGGGGGGCGTCTTCTTCGGGATGGACAGGCCCCTAAGCTGCG

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                     ACTCTGCTCTGAGCAGCCTGGGATGCTGAACTCTTCAGAGAGATTTTTTATAGAGAGAT
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                                              ATCCCAGGGCATAGGACTTGCAGGTTCCTAGGAGCAGGATCTCCCATCGCACGTGCT
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Unclassified.

E 1 (bases 1 to 1300)
S Mang, Y. and Spellman, M.W.
O-fucosyltransferase
O-fucosyltransferase
AL Patent: US 6270897-A 6 07-AUG-2001;
Location/Qualifiers
1300 "...*rnown" NAM"
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Sequence 6 from patent US 6270987.
AR163452. GI:16234057
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Best Local Similarity 99.99
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Pred. No. 2.7e-284;
0; Mismatches 1;
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                                                     17-DEC-1997 JP 1998532877
31-JAN-1997 US 08/792498,26
G WANG, MICHAEL W SPELLWAN
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
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1. 1300
/ organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                 JP 2001527389-A/2
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Patent: JP 2001527389-A 2 25-DEC-2001;
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	OY 361 GAAGGAAACCCTTTGGCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 420	Qy 421 CTITITACAGGCAITICCTICAGTGCTICCTACAGAGAACAATGGAGCCAGAGAITITCT 480	Qy 481 CCAAAGAACATCCGGTGCTTGCCCTGCCAGAGCCCCAGCCCAGTTCCCCGTCCTAGAA 540	Qy 541 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAG 600	Oy 601 GCCCAGAFTCATGCCCACCTTGTCCGGCCCTATGTGGCCATTCATCTGCGCATTGGCTCT 660	Oy 661 GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGACTGCAGGCTCGCACTTCATGGCC 720	Oy 721 TCTCCGCAGGGGGAGGGGCGCCCCCCCCCCCCCCCCCCC	
	Oy 841 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900	Qy 901 AAAGGGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 960	Qy 961 CTCGGCCAAGCCGACCACTTTAITGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020 Db 1096 CTCGGCCAAGCCGACGACTTTAITGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1155	Oy 1021 CGGGAGCGGGACCTCCAGGGGAGCCGTCTTCTTCGGCATGGACAGGCCCCCTAAG 1080 Db 1156 CGGGAGCGGACCTCCAGGGAGGCGGTCTTCTTCTTCGGCATGGACAGCCCCCTAAG 1215	Oy 1081 CTGCGGGACGAGTTCTGGTCGGGGGGCCCCGGACCCTCTGATCCTGGAGGGACCAG 1140	Qy 1141 AGTCTGADCTTCCTTCCAGCAG 1165 Db 1276 AGTCTGAGCTGCTTCCAGCCAG 1300	## ## ## ## ## ## ## ## ## ## ## ## ##	. Qy 241 AGCTIGGAGGAITTCAIGGAGAAGCIGGCACCCACCACTGGCCCCCTGAGAAGCGGGIG 300

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CTGGGCCAAGCCGACTATATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACACGCTCTTC
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                                                                                                                                                                                          AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC
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                                      TCTCCGCAGTGTGTGGGCTACAGCCGCAGCACACGGCCCCCCTCACGATGACTGC
                                                                                          CTGCCTGACCTGAAGGAGTCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGGATGCC
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                                                                                                                                   CAGICGGICTACGIIGCIACIGAIICCGAGAGIIAIGIGCCIGAGCICCAACAGCICTIC
                                                                           CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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Pred. No. 2.8e-267;
0; Mismatches 1; Indels 0;
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PE Corporation (NY) (US)
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CQ727777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                    'organism='Unidentified'
                                                                                      08/792498, 26-NOV-1997
                                                                                                                                                                                                                                                                                                                 72.7%; Score 1100; DB 6; I. larity 100.0%; Pred. No. 3.4e-268; Conservative 0; Mismatches 0;
                                                                                                                                                                         Location/Qualifiers
 Patent: JP 2001527389-A 9 25-DEC-2001;
                       Unidentified
JP 2001527389-A/9
JS-DEC-2001
17-DEC-1997 JP 1998532877
31-JAN-1997 US 08/792498,26-06
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single,
Topology: Linear;
Topology: Linear;
Co-fucosyltransferase
Key
Source
1.01100

    .1100
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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          GENENTECH INC
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PP 17-DEC-193
PR 31-JAN-194
PC C12N15/54
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; But Mammalia; Butheria; Primates; Catarrhini; Hominidae; Palattinez-Duncker,I., Mollicone,R., Candeller,J.J., Bret Oriol,R. A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases, and alpha6-fucosyltransferases phylogeny and identification of conserved peptide motification of conserved peptide motifications of fucosyltransferases unpublished 3 (bases 1 to 1167) Oriol,R. Direct Submission	JOURNAL Submitted (06-JUL-2004) Oriol R., USO4, Inserm, 16 Av. Paul PEATURES Vailant-Couturier, 94607, FRANCE Location/Qualifiers 1. 1167 / mol_type="mRNA" roglodytes" / mol_type="mRNA" roglodytes" / gene //gene="fut12" CDS 1. 1167 / qene="fut12"	/function="adds fucose to Ser or Thr" /note="potut1" /codon_start=1 /product="protein-O-fucosyltransferase 1" /protein_id="cAH03712.1" /db xxef="d1:5057070" /translation="MGAAMARPLSVSFLILLILPLPGMPAGSWDPAGYLLYCPCMGRF GNQADHFLGSLAFAKLINFTLAVPPWIEYQHKRPFTNILWSYQKYFKLEPLQAYHRV ISLEDPMEKLAPTHAPPEKRAVAYCEVAAQRSBDKKTCPMKRGMPAGSFWDQFHVSFN	X V V DE E	Matches 1091; Conservative U; Mismatches 7; Indels U; Gaps 1 ArdCCCGCGGGCTCCTGGGACCCGGCGGTTACCTGCTCTACTGCCCCTGATGGGGCGC 60 1	Db 130 TTTGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 189 Oy 121 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGGATCACAAGCTCTTTCACCAACCTC 180 Db 190 ACCTTGGTTGCTCCTTGGATTGAGTACCAGGATCACAAGCTTTTCACAACCTC 249 Oy 181 CATGTGCTAACAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGTCATC 240 Db 250 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATC 309	QY 241 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCTGAGAAGCGGTG 300 Db 310 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCTGGCCCCCTGAGAAGCGGTG 369 QY 301 GCATACTGTTGAGGAGCCGCGAGCCAGCTGACCCCTGAGAAGCGGTG 369 Db 370 GCATACTGTTGAGGCGCAGCCAGATAAGAAGACCTGCCCCTGAAG 369 Db 370 GCATACTGCTTTGAGGTGCCCAGCGAGCCCAGATAAGAAGCCCCATGAAG 429 QY 361 GAAAGGAAACCCCTTTGGCCCATTCTGGGAAGCCCAGATAAGAAGACGTGCCCCATGAAG 420
Db 250 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATC 309	Qy 541 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGCCCAGCCC	Db 670 GCCCAGATTCATGCCACCTTGTCCGGCCCTATGTGGCGTTCATCTGGCGTTTTGTTTTGTTTTTTTT	CTGCCTGACCTGAAGGAGTCCAGAGGCTGTGAAGCTCTGGGTGAGGT [QY 901 AAAGGGAAGGTGAAGGTGGTGAAGCCTGAAGGCCGAGGTGGACCTGTACATC 960 Db 1	Qy 1021 CGGGAGCGGACCTCCAGGGAGGCCGTCTTCTTTCTTCGGCATGGACAGGCCCCCTAAG 1080 Db	RESULT 15 AJ781500 LOCUS AJ781500 DEFINITION Pan troglodytes mRNA for protein-O-fucosyltransferase 1 (fut12 DEFINITION Pan troglodytes mRNA for protein-O-fucosyltransferase 1 (fut12 BGES) ACCESSION AJ781500 AJ7

AG 489	T 480	 T 549	LA 540	609 DV	009 b	699 5v	77 660	T 729	720	L 789	ic 780	L 849	C 840	ا اد 909	006 5	ا در 969	096 5	ا در 1029	G 1020	ր 1089	G 1080	 G 1149			
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430 G	421 C	490 G	481 C	550 C	541 G	610 G	601 G	670 G	661 G	730 G	721 T	790 T	781 C	850 C	841 C	910 C	901 A	970 A	961 C	1030 C	1021 C	1090 4	1081 C	1150 C	
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Search completed: November 9, 2005, 07:59:57 Job time : 6834.38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

November 8, 2005, 23:23:13; Search time 883.842 Seconds (without alignments) 10140.369 Million cell updates/sec Run on:

US-09-774-954-1

1514 1 ATGCCCGCGGGCTCCTGGGA......TTTTGAAAATCATTGAATTC 1514 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

N Geneseq 16Dec04:* Database :

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aav65632 Human hea Aav65633 Plasmid c Acn40746 Tumour-as Adf81754 Leukaemia Aak51510 Human pol Aak52494 Human pol Aav65634 First Eco Aad07629 Human sec Aak79915 Human rep Ach35532 Human end Ach35225 Human end Ach3225 Human end Ach3225 Human end Ach3224 Human sec Abl13347 Drosophil Abl13394 Drosophil Abl13952 Drosophil Abl13952 Drosophil Abl13953 Drosophil Abl13953 Human sec Abl13954 Human sec Abl139554 Human sec Abl139554 Human sec Abl139554 Human sec Abl1395554 Human sec Abl139554 Hum
SUMMARIES	AAV65632 AAV65633 ACN40746 ABCB1754 AAK51510 AAK52494 AAK52494 AAV79915 AAV79915 AAL03344 AAL03344 AAL13347 ABL13947 ABL13947 ABL13947 ABL13994 ABL13994 ABL13994 ABL13994 ABL13994 ABL13994
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Ada71938 Rice gene		Aca31561 Prokaryot	Aad08215 Human gen	Aah97782 Murine 7-	Adt44716 Bacterial	Adq80232 Brain-spe	Adg84111 Human tum	Adb75488 Prostate	Aav65637 Primer am	Aav65635 Northern	Ada69815 Rice gene	Aca43606 Prokaryot	Adc37615 Human nuc	Abd01472 Pseudomon	Aaa61286 Human sec	Ada40219 Human sec	Add37708 Human sec	Ada56378 Gene enco	Abd01484 Pseudomon	Adc16737 Human mod	Aah15283 Human cDN	Aas44695 Human ful	Aas01567 Human sec	Adil6595 Human NOV	
ADA71938 ,	ADA71938	ACA31561	AAD08215	AAH97782	ADT44716	ADQ80232	ADQ84111	ADB75488	AAV65637	AAV65635	ADA69815	ACA43606	ADC37615	ABD01472	4AA61286	ADA40219	ADD37708	ADA56378	ABD01484	ADC16737	AAH15283	AAS44695	AAS01567	ADI16595	
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3.3	3.1	2.8	2.7	2.7	2.7	2.7	2.7	2.7	5.6	5.6	5.6	5.6	5.6	5.6	5.6	9.8	5.6	5.6	5.6	٠		9.7	5.6	5.6	
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21	c 22	23	c 24	c 25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45 ,	,

ALIGNMENTS

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Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                                       O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                                                                                                         Location/Qualifiers
1. .1100
/*table actively expressed O-fucosyltransferase sequence is claimed for in claim 9"
1. .1098
/*tag= a /product= "human heart O-fucosyltransferase"
                                                                                  Human heart O-fucosyltransferase encoding DNA.
                    BP.
                                                                                                                                                                                                                                                                                                                          97US-00792498.
97US-00978741.
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                   AAV65632 standard; DNA; 1514
                                                            16-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                              Wang Y, Spellman MW;
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P-PSDB; AAW80571.
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26-NOV-1997;
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                                        AAV65632;
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RESULT 1
           AAV65632
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GTGCTTTCTGCTCTTCTGGGAATTTCTCACACTGGCAAAGCAGTCCAGCCTCCGTCTTCT 1380
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4140. .5333
/*tag= a
/note= "insert coding for human O-fucosyltransferase."
/*tag= b
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                                      CAGICGGICTACGITGCTACTGAITCCGAGAGITAIGTGCCTGAGCTCCAACAGCTCTTC
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781 CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
                         CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid construct for expression of human O-fucosyltransferase.
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                                   This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polygeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of officosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
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                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Score 1514; DB 2; Length 1514;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1514; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                      Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
                 Fig 12A; 90pp; English
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CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCCAGCTTCCCCGTCCTAGAG
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상염
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                                                                                                                               Tumour-associated antigenic target (TAT) cDNA DNA326813, SEQ ID NO:5725.
                                                                                                                                                           Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; call proliferative disorder; breast cancer; colorectal cancer; lung cancer; overian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
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99.9%; Pred. No. 0;
ative 0; Mismatches 2; Indels 0; C
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                                ACN40746 standard; cDNA; 5218 BP.
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Best Local Similarity 99.99
Matches 1512; Conservative
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P-PSDB; ABM82223.
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 of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, for the preparation of a medicament for treating leukaemia.
                                                          Sequence 5266 BP; 1280 A; 1278 C; 1331 G; 1346 T; 0 U; 31 Other;
                                                                                      DB 10; Length 5266;
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Pred. No. 0;
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Best Local Similarity 99.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a
AGTCTGAGCTGGTCCTTCCAGCCAGGCCTGGCAGCCAGAGGTGCTCCGGGATTGCAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukaemia-related DNA sequence #2310
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                                                                                           CTGCGGGACGAGTTCTGATTCTGGCCGGAGCACCAGACCCTCTGATCCTGGAGGGACCAG 1140
                                                                                                                                                                                                                                                                                            GIGCTITCIGCICTICTGGGAAITTCICACACIGGCAAAGCAGTCCAGCCTCCGICITCT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCTTTCTGCTCTTCTGGGAATTTCTCACACTGGCAAAGCAGTCCAGCCTCCGTCTTCT 1511
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                                                                                                                                                                                                       AGTOTGAGCTGGTCCTTCCAGCCAGGCCTGGCAGAGCTGCTCCGGGGATTGCAAACT 1200
                                                                                                                                                                                                                         AGTCTGAGCTGGTCCTTCCAGCCAGGCCTGGCAGCCAGGGTGCTCCGGGATTGCAAACT 1331
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; 2000US-00560875.
; 2000US-0059075.
; 2000US-00654936.
; 2000US-0063561.
; 2000US-0063351.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetleetides and polypeptides are useful in game therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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266 TGCTAAACCGTACCTTGGATTGAGTACAAGCACCACCTCCTT
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   Xu C, Cao
Chen R,
Asundi V, Zhou P, Xı
J, Zhang J, Ren F,
Goodrich R;
                                                                                                                                                                                          Nucleic acids encoding polypeptides with in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                          Claim 1; Page 638-642; 6221pp; English.
Drmanac RT, P
Wang D, Wang J
Wejhrman T, G
                                                                                                           WPI; 2001-476283/51.
P-PSDB; AAM78377.
Tang YT, Liu C,
Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomedulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; sa

2001WO-US004098

05-FEB-2001;

09-AUG-2001

WO200157190-A2. Homo sapiens.

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03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00693325.
30-NOV-2000; 2000US-00693325.
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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

invention relates to polynucleotides (AAK51456-AAK53435) and

Claim 1; Page 4424-4425; 6221pp; English.

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Y, Wang

Cao R, chen

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Drmanac RT, Asundi V, Zhou P, Xv Wang D, Wang J, Zhang J, Ren F, Wejhrman T, Goodrich R;

Liu C, nao QA, W Yang Y,

Zhao

Tang YT, Ma Y, Zh Xue AJ,

(HYSE-) HYSEQ INC

2001-476283/51.

P-PSDB; AAM79361

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concided polypeptides (AAA/832)-AAA880302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, hemantopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEO ID NO 2110 (AAK528B1), 2111 (AAK528B2) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                                                                                                                                                                                                                                                Sequence 4850 BP; 1142 A; 1218 C; 1244 G; 1246 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            4; Length 4850;
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Pred. No. 0;
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Mismatches
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Best Local Similarity
Matches 1459; Conserv
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Human polynucleotide SEQ ID NO 2023

(first entry)

06-NOV-2001

AAK52494

AAK52494
ID AAK5
XX AAK5
XX AAK6
DT 06-1
XX
DE HUE

AAK52494 standard; cDNA; 4850

RESULT 6

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This represents a first EcoR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial cDNA encodes for a protein of unknown function from wpoblast cel line KG-1. The invention provides a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase.
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1526 CTCCGTCTTCTGGTCCACTCTGAGCAGCCTGGGATGCTGAACTCTTCAGAGAAT
                                                                                                                                                                                                                                                                                                                                                                             O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                              First EcoR1 nucleotide fragment of human KIAA0180.
                                                                                                            1490 GIGGITITIGAAAATCATIGAATIC 1514
                                                                                                                                GTGGTTTTTGAAAATCATTGAATTC 1670
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P-PSDB; AAW80577.
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26-NOV-1997;
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      GCCCCATGAAGGAAAGCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCA
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occurring L-amino
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                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; fimune system disorder. ALS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; penanoy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; chromosome 3;
                                                                     1261 TTCTGCTCTTCTGGGAATTTCTCACACTGGCAAAGCAGTCCAGCCTCCGTCTTCTGGTCC
                                                                                                                                               TTCTATAATTTTGATACAAGGTCATGACTATCCTAGAACTCTCTGTGGTTTTTTGAAAATC
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                         ACTCTGCTCTGAGCCAGCCTGGGATGCTGAACTCTTCAGAGAGATTTTTTATAGAGAGAT
              ATCCCAGGGCATAGGACTTGCAGGTTCCTAGGAGCAGGAGCATCTCCCATCGCACGTGCT
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/product= "Human secreted protein precursor"
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/transl_except= (pos:13. .15, aa:Xaa)
/transl_except= (pos:442. .444, aa:Xaa)
/note= "Xaa equals any of the naturally occuacids; CDS does not include start codon"
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                                GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTGGCATA
                                                                                                             AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTT
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                                                                                   Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
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Matches 859; Conservative
            Ruben SM, Komatsoulis
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 34727; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially

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20000US-0186558P.
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cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietid antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                  1072 CCCCTAAGCTGCGGACGACTTCTGATTCTGGCCGGACCACAGACCCTCTGATCCTGG
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                                                                                                 Sequence 10331 BP; 2718 A; 2405 C; 2599 G; 2609 T; 0 U; 0 Other;
                                                                                                                                     4; Length 10331;
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                                                                                                                                   Match 40.2%; Score 608.6; DB 4; Length Local Similarity 98.6%; Pred. No. 4e-166; Length es 614; Conservative 0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                     951
              system antigen is condition.
                                                                             The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                               Sequence 10331 BP; 2718 A; 2405 C; 2599 G; 2609 T; 0 U; 0 Other;
                                                                                                                                                                                          40.2%; Score 608.6; DB 4; Length 10331; 98.6%; Pred. No. 4e-166; ive 0; Mismatches 9; Indels 0;
                                                   Disclosure; SEQ ID NO 6032; 1297pp + Sequence Listing; English.
              Isolated nucleic acid molecule encoding a reproductive used in preventing, treating or ameliorating a medical
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Best Local Similarity 98.6
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430 CATAGGACTTGCAGGTTCCTAGGAGCAGGAGCATCTCCCATCGCACG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human endothelial cell cDNA #358.
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(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Labat I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-615964/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACH32225;
                         1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by Mybridiaenton). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data cottained in electronic format directly from USPTO at sequence that was sequence. The sequence that seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
Human; 88; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 HGATGCTGAGCNCTAGAGATATGTGCCTGAGCTCC-ACAGTTCTTCAAAGGGAAGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 GGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 477 BP; 95 A; 141 C; 142 G; 97 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 22744; 44pp; English.
                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                              30-JUL-2001; 2001US-00918995.
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Best Local Similarity 98.11
Matches 458; Conservative
                                                                                                                                                                                                                                                                                                                                                            (LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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                                                                                                                                                                                                                                                                                                                               (DRMA/) DRMANAC R T.
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                                                                                                                           US2003073623-A1.
                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                         (LABA/)
(STAC/)
(DICK/)
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH56811, whose sequence was determined by the technique of SBH (sequencing by hybridiaation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences care useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this pattent did not form part of the printed specification, but was sequence to the printed in electronic format directly from USPTO at sequence. Use sequence. The sequence contained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynuclectide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
Human, ss, sequencing by hybridisation, SBH, expressed sequence tag, EST, genome mapping, biodiversity, genetic disorder.
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or
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                                                                                                       928 AAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCACTTTATTGGC
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                                                      TCAAAGGGAAGGTGAAGGTGGTGAGCCTG
                                                                                                                                  91 AAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCACTTTATTGGC
                                                                                                                                                               AACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGAGCGGGACCTCCAGGGGAGGCCG
                                                                                                                                                                                          151 AACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGAGCGGGACCTCCAGGGGAGGCCG
                                                                                                                                                                                                                    TCTTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCGGGACGAGGTTCTGATTCTGGCCG
                                                                                                                                                                                                                                               211 TCTTCTTTCTTCGGCATGGACAGGCCCCTAAGCTGCGGGACGAGTTCTGATTCTGGCCG
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                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      canine microarray; drug screening; toxicity assay;
environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                           ;
 Length 479;
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel canine microarray-related DNA sequence SeqID8126.
Score 441; DB 9; L
Pred. No. 6.9e-118;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTCCTAGGAGCAGGAGCATCTCCCATC 1316
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                                                   868 GAGAGTTATGTGCCTGAGCTCCAACAGCTCT
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29.1%;
ilarity 98.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-561890/54.
            Similarity
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                      444;
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Query Match
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This invention is related to a novel isolated canine mucleic acid
sequences and the construction of canine microarrays containing a
significant portion of the canine genome. The isolated canine nucleic
alignificant portion of the canine genome. The isolated canine nucleic
call provide to the invention may be useful for drug screening and
toxicity assays. The invention may be useful for drug screening and
cupacity including toxicity, of a compound, pharmaceutical agent or
cupacity including toxicity, of a compound, pharmaceutical agent or
cupacity including toxicity, of a compound, pharmaceutical agent or
cuseful for detecting genes that are up. or down-regulated in canines in a
disease state. The sequences are useful as diagnostic agents or markers
to detect a cellular response in a sample individually or as part of a
gene expression profile. It is also useful as a target for agents that
compound near expression or activity. The database is useful for
producing electronic Northerns that allow the user to determine the cell
type or tissue in which a given gene is expressed and to allow
determination of the abundance or expression level of a given gene in a
particular tissue or cell. The methods are useful for determining the
similarity of a toxic response to one or more individual compounds. The
methods are useful for predicting at least one toxic response or the
similarity of a toxic response to one or more individual compounds.
The methods are useful for predicting at least one toxic response or the
similarity of a toxic response to one or more individual compounds.
The methods are also useful for predicting or elucidating
the toxins. The methods are also useful for predicting or elucidating
the potential cellular pathways influenced, induced or medulated by the
company or test agent due to the similarity of the expression profile individual companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 610 BP; 155 A; 171 C; 149 G; 129 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production of a canine microarray of the invention.
                                                                SEQ ID NO 8126; 41pp; English.
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1; DB 13; Length 610; Indels Score 406.2; DB 13; Pred. No. 1.1e-107; 0; Mismatches 54; 26.8%; 89.0%; Query Match 26.8 Best Local Similarity 89.0 Matches 446; Conservative CACCAACCTCCATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCA

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11.0%; Score 166.4; DB 4; Length 12

Best Local Similarity 51.5%; Pred: No. 1.7e-37;

Matches 563; Conservative 0; Mismatches 486; Indels

Matches 563; Conservative 0; Mismatches 486; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therespectics, and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 36320; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                    Myers EW
                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                     23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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P-PSDB; ABB69843.
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9, 2005, 04:43:18 completed: November 887.842 secs time

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Sequence 12127, A
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Sequence 14353, A
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1: /cgn2 6/ptodata/1/ina/5A COMB.seq:*

2: /cgn2 6/ptodata/1/ina/6B COMB.seq:*

3: /cgn2 6/ptodata/1/ina/6A COMB.seq:*

5: /cgn2 6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2 6/ptodata/1/ina/bcTuS COMB.seq:*

5: /cgn2 6/ptodata/1/ina/pcTuS COMB.seq:*
           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-370-767-14353

US-09-270-767-13022

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US-09-940-016-16285

US-09-940-016-16285

US-09-902-540-1217

US-08-978-741-10

US-08-978-741-10

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US-08-978-741-10

US-09-912-791A-88

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Sequence 11941, A
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Sequence 13025, A
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US-09-940-016-13678
US-09-940-3168-1
US-09-252-991A-11943
US-09-252-991A-11977
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US-09-949-016-13025
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US-08-404-3548-1
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US-10-237-551-191
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MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winter in Genentech)
CURRENT APPLICATION TOWARE: US/08/978,741
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION OFF: 315
ATTORNEY/ACENT INFORMATION: NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9881
INFORMATION POR SEQ ID NO: 1:
SEQUENCE: CHARACTERISTICS:
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Patent No. 6100076

GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION:
CORRESPONDENCEs: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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TOPOLOGY: Linear
US-08-978-741-1
1411529
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Best Local Similarity
Matches 1514; Conserv
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	RESULT 2 US-09-313-729A-2 is equence 2, Application US/09333729A is equence 2, Application US/09333729A is patent No. 6270987 is ferrex. INFORMATION: is APPLICANT: Wang, Yang is APPLICANT: Spellman, Michael W. is TITLE OF INVEXTION: O-PUCOSyltransferase is FILE REFERENCE: pl041PlD1-Substitute is TITLE OF INVEXTION: UNMBER: US/09/33,729A is CURRENT FILING DATE: 1999-10-15 is PRIOR FILING DATE: 1999-11-26 is NUMBER OF SEQ ID NOS: 21 is DENGTH: 1514 is TYPE: DNA is TYPE: DNA is ORGANISM: Homo Sapien	Query Match 100.0%; Score 1514; DB 3; Length 1514; Best Local Similarity 100.0%; Pred. No. 0; 0; Mismatches 0; Indels 0; Gaps 0; QY 1 ATGCCGGGGCTCTGGGACCCGGCTTACTGCCCTCTGCATGGGGCG 60 Db 1 ATGCCGGGGCTCTGGGCCGGTTACTGCTCTGCTCTGCTGTGGGGCG 60 QY 61 TTTGGGAACCGGGCCGGTTACTGGCTTTGCTGCTGTGTGGGGCG 60 Db 61 TTTGGGAACCGGGCGATCACTTTGGGCTTTTGCAAAGCTGTAAACCGT 120 Db 61 TTTGGGAACCAGGCGCGATCACTTGGGATTTGCAAAGCTGTAAACCGT 120 Db 61 TTTGGGAACCAGGCGCATCACTTGAGTACCAGCATTTGCAAAGCTGTAAACCGT 120 QY 121 ACCTTGGCTGTCCTTGGATTGAGTACCAGCATTACAAGCTGCTAAACCTC 180 Db 121 ACCTTGGCTGTCCTTCGATTGATACAGACTACACAGCATTACACAACCTC 180 QY 181 ACTTGGTGCTCTCCTACGATTCAAGCTGGAACCCCTCCAGGCTTACCATCGGGTCATC PB 181 CATGTGTCCTACCAAGATACTTCAAGCTGGAACCCCTCCAGGGTTACCATCGGGTCATC QY 241 AGCTTGGAGGATTCAAGCTGGAACCCCCCCTCCAGGGTTACCATCGGGTCATC QY 241 AGCTTGGAGGATTCAAGCTGGACCCCCCCTCCAGGAACCGCTCTCAGAAACCGGTGAACCCCCTCCAGAACACGGTGAACCCCCTCGAGAACCGGGTGAACACCCCTCCAGAACACGGTGAACCCCCTCGAGAACACGGTGAACACCCCTCCAGAACACGGTGAACACCCCTCCAGAACACGGTGAACACCCCTCCAGAACACGGTGAACACCCCTCCAGAACACACAC
61 TTTGGGAACCAGGCGATCACTTCTTGGGCTCTTGGCATTTGCAAAGCTGCTAAACCGT 120 61 TTTGGGAACCAGGCCGATCACTTCTTGGGCATTTGCAAAGCTGCTAAACCGT 120 61 TTTGGGAACCAGGCCGATCATCTTGGGCTTCTTGGCAATTTGCAAAGCTGCTAAACCGT 120 121 ACCTTGGCTGTCCCTCCTTGGATTGGTACCAGGATCACAAGCCTCCTTTCACCAACCTC 180 121 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGGATCACAAGCCTCCTTTCACCAACCTC 180 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTCTTCACCAACCTC 240 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTCTACCATCGGGTCATC 240 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCAGGCTCTACCATCGGGTCATC 240 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCAGGGGTCATC 240 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGACCCCCTCAGGGTCATC 240 182 ACCTTGGAGGATTTCATGAAGAAGCTGGACCCCACTGGCCCCTTAACAAGCGGGTCA 300 183 ACCTTGGAGGATTTCATGAGAAGCTGGACCCCACTGACGCCCCATGAAG 360 184 ACCTTGGAGGATTTCATGGAAACCCCACCAACTAGAGCTGCCCCATGAAG 360 185 AAAGGAAAACCCCTTTGGCCCACTGGAACCCCATGAAG 360 186 AAAGGAAAACCCCTTTGGCCACTTTCTGGAATTTCAACAAGTCGGAG 420 187 AAAGGAAAACCCCTTTGGCCATTCTGGGATCAGTTTCAATGGAGATTTCAACAAGTCGGAG 420 188 AAAGGAAAACCCCTTTGGCCCATTTCTGGGATCAGTTTCAATGGAGATTTCTT 480 189 AAACTTTTAACAGGCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 420 181 AAACTTTTAACAGGCATTTCTTGAGAACCACAAATTTCT 480 181 AAACTTTTAACAGGCATTTCCTTACAGAGAACAATGGAGACCACAAATTTTCT 480 181 AAACTTTAACAGGCATTTCCTTACAGAGAACAACGAAAATTTTCT 480 181 AAACTTTAACAGGCATTTCCTTACACAAAACGAAACCACAAATTTTCT 480 181 AAACTTTAACAGGCATTTCCTTACACAAAAACGAAACCACAAAATTTCTT 480 181 AAACTTTAACAGGCATTTCCTTACAACAAAACGAAACCACAAAATTTTCTT 480 181 AAACTTTAACAGGCATTTCCTTACAACAAAACGAAACCAAAATTTTCTT 480 181 AAACTTTAACAAGCATTTCCTTACAACAAAACGAAACCAAAATTTTCTT 480 181 AAACTTTAACAAGCATTTCCTTACAAAAAACGAAACCAAAATTTTCTT 480 181 AAACTTTAACAAGCAAAATTTCCTTACAAAAAACGAAAATGGAAAATTTTCTTAAAAAAAA	481 CCAAAGGAACATCCGGTGCTTGCCAGGAGCCCCAGGTTCCCCGTCCTAGAA 540 481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGGTTCCCCGTCCTAGAA 540 481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGGTTCCCCGTCCTAGAA 540 481 CAACACAGGCCACTACAGAAGTACATGGTATGGTCAAACAGGTGCAGAAGAGCGGAGAG 600 541 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAAACAGACAG	18 CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGATGCC 840

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTE: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbarin (Genentech) CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997 CLASSIPRCATION 1435 PRIOR APPLICATION DATA: APPLICATION NATA: APPLICATION NUMBER: 08/792498
 GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
COUNTY: SOuth San Francisco
STATE: California
                                                                                                                                                                                                                                                                              PILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: STOODOGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REPERENCE/DOCKET NUMBER: P1041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 130 Dase pairs
TYPE: NUCleic Acid
STRANDEDNES: SINGle
                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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Sequence 4, Application US/08978741 Patent No. 6100076

US-08-978-741-4 ; Sequence 4, Appl ; Patent No. 6100

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CGGGAGCGGGACCTCCAGGGGAGGCCGTCTTCTTCGGCATGGACAGGCCCCCTAAG 1080 TIGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900 AGGGGGGGGCCGAAGCCTGAGGGGCCCAGGTCGACCTGTACATC 960 ACCACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAG 1020 ö AGGTGGCAGCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360 315 240 rcatggagaagctggcacccacccactggccccttgagaagcgggtg 300 420 555 480 615 CAGTGCTTGCCCTGCCAGAGCCCCAGCCCAGTTCCCCGTCCTAGAA 540 PACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAG 600 099 720 855 780 918 AGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840 195 120 255 TICCTIGGATIGAGIACCAGCATCACAAGCCICCTITCACCAACCIC 180 375 795 60 CCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT TCTTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC AGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATC TTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT Gaps . 0 1; Indels 9.9%; Pred. No. 0; ve 0; Mismatches

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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333, 729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 09/798, 741
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 FTLING DATE: 26-No. 6100076-1997 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: 08/792498 FTLING DATE: 39,044 RECISTRATION NUMBER: 99,044 RECISTRATION NUMBER: 99,044 REFERRICE/DOCKET NUMBER: 91041P1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: 15: SEQUENCE CHARACTERISTICS: LENGTH: 1100 Dase pairs SEQUENCE CHARACTERISTICS: LENGTH: 1100 Dase pairs STRANBENDEDNES: Single
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
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Pred. No. 6.1e-41;
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TITLE OF INVENTION: NUCleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                   RESULT 10
US-09-270-767-14353
Sequence 14353, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
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Best Local Similarity 51.6%;
Matches 564; Conservative (
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 1997-11-26
             ; NUMBER OF SEQ ID NOS: 2; SEQ ID NO 16; LENGTH: 1100; TYPE: DNA; ORGANISM: Homo Sapien US-09-333-729A-16
PRIOR FILING DATE: 199
NUMBER OF SEQ ID NOS:
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE PEPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER: OF SEQ ID NOS: 62217

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 28905

LENGTH: 998
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TITLE OF INVENTION: No.1eic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: No.1eic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13022
LENGTH: 2034
ACTITATCGGCAACTGTATATCCTCTTACTCGCCATTCGTAAAAAGGGAACGAGATGTGC
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                                                              TCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCCAGTCGGTCTACGTTGCTA
                                                                                                      288 CCATTAAGAACGTGCGCCAAACTCAGCCGGACAAACGAAATCAGTTTTCGTGGCGT
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60.2%; Pred. No. 2.7e-07;
iive 0; Mismatches 64;
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Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 28905, Application US/09270767; Patent No. 6703491; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA; ORGANISM: Drosophila melanogaster
US-09-270-767-28905
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US-09-270-767-28905/c
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US-09-270-767-13022/c
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Sequence 30507, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Morieic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
LENGTH: 722
                                                                                                      CGGGAGAGCCCAGATTCATGCCCACCTTGTCCGGC---CCTATGTGGGCATTCATCTGC
                                                                                                                                                                                                                                                                                                               TGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCT
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49.5%; Pred. No. 1.7e-08;
Live 0; Mismatches 218; Indels 12;
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CRGANISM: Drosophila melanogaster
US-09-270-767-30507
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US-09-270-767-30507
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is Sequence 1212.7, Application US/09949016

j Batent No. 681239

i GENERAL INFORMATION:

j APPLICANT: UNTER, J. Craig et al.

i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR SEQ ID NOS: 2070102

SEQ ID NOS: 2070102

SEQ ID NOS: 2070102

SEQ ID NO 12127

LEMERAL OF SEQ FOR WINDOWS VERSION 4.0
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Sequence 16285, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILLE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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                                                                                                     Query Match 3.9%; Score 58.6; DB 4; Length 2034; Best Local Similarity 60.2%; Pred. No. 4.4e-07; Matches 97; Conservative 0; Mismatches 64; Indels 0
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                      ORGANISM: Drosophila melanogaster
US-09-270-767-13022
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Best Local Similarity 100.C
Matches 56; Conservative
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US-09-949-016-16285/C
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ORGANISM: Human
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TYPE: DNA
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Sequence 6032, Apply Sequence 6032, Apply Sequence 1986, Apply Sequence 19437, Apply Sequence 19437, Apply Sequence 18160, Apply Sequence 18160, Apply Sequence 18169, Apply Sequence 18169, Apply Sequence 17287, Apply Seq

Sequence 236, App Sequence 1944, Sequence 1941, A Sequence 3, Appli Sequence 114097, Sequence 112, App Sequence 112, App Sequence 12, App Sequence 12, App Sequence 12, App Sequence 13, App Sequence 31476, A Sequence 31476, A Sequence 31, Appl Sequence 31476, A Sequence 31, Appl Sequence 120, Appl Sequence 1

Scoring table:

Searched:

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Perfect score:

Sequence:

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-774-954-1
Sequence 1, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Pucosyltransferase
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
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ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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2.7 114793
2.7 12036
2.7 2036
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Sequence 4752, Ap
Sequence 7, Appli
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Sequence 5, Appli
                                                                                                                      9, 2005, 08:00:04; Search time 1355.3 Seconds (without alignments) 9238.165 Million cell updates/sec
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(gnz 6/ptodata1//pubpna/US07 PUBCOMB seq:*
(cgnz 6/ptodata1//pubpna/US07 NEW PUB.seq:*
(cgnz 6/ptodata1//pubpna/US06 NEW PUB.seq:*
(cgnz 6/ptodata1//pubpna/US06 NEW PUB.seq:*
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(cgnz 6/ptodata1//pubpna/US09 NEW PUB.seq:*
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                  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-774-954-5
US-10-301-822-168
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Sequence 465, A Sequence 11732, Sequence 190, A Sequence 1 Sequence 4 Seguence

Sequence Sequence

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                             CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGTGTCTTGGTTGTGTGTCT
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        CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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US-09-774-954-5
US-09-774-954-5

JOHN CONDITION OF US20040241645A1

PUDIICATION NO. US20040241645A1

GENERAL INFORMATION:

TITLE OF INVENTION: O-Fucosyltransferase

CORRESPENDENCES: 17

CORRESPENDENCES: 17

CONDITION: ADDRESSE: Genentech, Inc.

STREET: 1 DNA WAS

CITY: South San Francisco

STREET: 1 DNA WAS

COUNTRY: USA

COUNTRY: USA

TIP: 34080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: Hab PC compatible

COMPUTER: Hab PC compatible

COMPUTER: Hab PC compatible

COMPUTER: WinPatin (Genentech)
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ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REPRERENCE/DOCKET NUMBER: P1041P1
TELEPHONE: 650/225-1489
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 Dass pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                          Query Match 100.0%; Score 1514; Best Local Similarity 100.0%; Pred. No. 0; Matches 1514; Conservative 0; Mismatches
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Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.;
APPLICANT: Guillemette, Tracy L.;
APPLICANT: Kamatkar, Shubhangi;
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.;
APPLICANT: Thibodeau, Stephen N.
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                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/978,741
FILING BATE: 26-00V-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGRYT INFORMATION:
NAME: SVODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                     Score 1512.4;
Pred. No. 0;
0; Mismatches
INT APPLICATION DATA:
PPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 11284 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.9%;
Matches 1513; Conservative
   CURRENT
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Sequence 4752, Application US/10956157
Publication No. US20050118625A1
GENERAL INPORATION:
APPLICANT: Wyeth
APPLICANT: WornTron: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH-
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
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   GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
                                                                                                                      CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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US-10-956-157-4752
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERARY OF COLON CANCER
FILE REFERENCE: MANDAIN-0.0292FNN
CURRENT APPLICATION NUMBER: US, 60/330, 971
PRIOR APPLICATION NUMBER: US, 60/339, 971
PRIOR APPLICATION NUMBER: US, 60/330, 978
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2002-05-50
NUMBER OF SEQ ID NUMBER: US, 60/381, 988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FREEESQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Length 5218;
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                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
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, LOCATION: (50)
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Publication No. US20040241645A1

GENERAL INFORMATION:

TITLE OF INVENTION: O-Fucosyltransferase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPTER READABLE FORM:
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FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-0AN-1997
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APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: <unknown>PRIOR APPLICATION DATA:
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                                                                                                       Score 1510.8;
Pred. No. 0;
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                                                                                                    Query Match
Best Local Similarity 99.9%;
Matches 1512; Conservative
SOFTWARE: Patentin version
SEQ ID NO 4752
LENGTH: 5218
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                                        ; TYPE: DNA
; ORGANISM: HOMO
US-10-956-157-4752
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US-09-774-954-4

| Sequence 4', Application US/09774954
| Sequence 4', Application No. US20040241645A1
| Publication No. US20040241645A1
| GENERAL INFORMATION:
| APPLICANT: Yang Wang, Michael W. Spellman APPLICANT: Yang Wang, Michael W. Spellman ITILE OF INVENTION: O-FUCOSYLTANSFERSES CORRESPONDENCE ADDRESSE: ADDRESSES: Genentech, Inc.
| STREET: 1 DNA Way
| CITY: South San Francisco STATE: California
| COUNTRY: USA TTD: 94080
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: MinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 30-Jan-2001
CLASSIFCATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: US/08/978,741
APPLICATION NUMBER: US/08/978,741
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                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                           DB 11; Length 5009;
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91,041P1
FELEPON INFORMATION
FELEPON E 650/52-1489
FELEPON E 650/52-1489
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FYPE: NUCLEIC ACID
STRANDENCE CHARACTERISTICS:
FYPE: NUCLEIC ACID
STRANDENCES: SINGLE
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-774-954-7
                                                                                                                                                                                                        Query Match
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches
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                     CTGCCTGAACGTGAAGGAGTCCAGAGGGCTGTGAAGCTCTGGGTGAGGGTGCATGGATGCC
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                                                                  CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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STREET: 1 DNA WAY

CITY: SOUTH SAN Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ISM PC computeR
COMPUTER: ISM PC compuTER
COMPUTER: I
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Publication No. US20040241645A1
GENERAL INFORMATION:
TYPICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1041P1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 AGTCTGAGCTGGTCCTTCCAGCCAG 1165
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INFORMATION FOR SEQ ID NO: 16:
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STRANDEDNESS: Single
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US-09-774-954-16
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FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-5A-1997
ATTORNEY/AERT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-1489
TELEFAX: 650/25-1489
TELERGARATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1300 base pairs
TYPE: Nucleic Acid
STREE NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.8%; Score 1163.4; Best Local Similarity 99.9%; Pred. No. 0; Matches 1164; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6032
LENGTH: 10331
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Best Local Similarity 98.6%; Pred. No. 5.4e-186;
Matches 614; Conservative 0; Mismatches 9;
                                                                                                                                  RESULT 8
US-09-764-891-6032
Sequence 6032, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
                                                                      CTGCGGGACGAGTTCTGATT 1100
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-891-6032
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                                      DB 11; Length 1100;
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                                   Query Match 72.7%; Score 1100; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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JS-09-774-954-16
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                                                                                                                                                                                                                                                              Score 471.4; DB 22; Lengthered. No. 9e-142;
O; Mismatches 1; Indels
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TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 22744
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US-09-918-995-22744
US-09-918-995-22744, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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LOCATION: (1) ... (477)
OTHER INFORMATION: n = A,T,C or G
     CURRENT FILING DATE: 2004-10-04 NUMBER OF SEQ ID NOS: 319805 SOFTWARE: Patentin version 3.2 SEQ ID NO 4751
                                                                                                                                                                                                                                                                 31.1%;
99.8%;
                                                                                                                                                                                                                                                              Query Match 31.1
Best Local Similarity 99.8
Matches 472; Conservative
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                                                                                                                                                                                                         US-10-956-157-4751
                                                                                                                      LENGTH: 1506
                                                                                                                                                 TYPE: DNA ORGANISM: 1
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                                                                                                                                                                              Sequence 9986, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHATIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM THOLO81)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOPTWARE: Patentin Version 3.2
SEQ ID NO 9986
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APPLICANT: Wounts, William
APPLICANT: Wounts, Wounts, William
APPLICANT: Wounts, Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, Wou
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Pred. No. 8.7e-142;
0; Mismatches 1; Indels 0;
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                                      6727 GGTTTTTGAAAATCATTGAATTC 6749
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Best Local Similarity 99.8%;
Matches 472; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9986
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US-11-097-143-18161

Sequence 18161, Application US/11097143

Publication No. US2005020858A1

GENERAL INFORMATION:

APPLICANT: Venter. J. Craig

APPLICANT: Venter. J. Craig

APPLICANT: Venter. J. Craig

TITLE OF INVENTION: DRESCPILLA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

PRIOR APPLICATION NUMBER: 60/157, 332

PRIOR PELING DATE: 1999-10-19

PRIOR PELING DATE: 1999-10-28

PRIOR PELING DATE: 1999-10-19

PRIOR PELING DATE: 1999-10-19

PRIOR PELING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/164, 769

PRIOR APPLICATION NUMBER: 60/164, 769

PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 2000-01-12, 28

PRIOR PELICATION NUMBER: 60/1164, 331

PRIOR PELICATION NUMBER: 60/1164, 331

PRIOR PELICATION NUMBER: 60/101, 637

PRIOR PELICATION NUMBER: 60/191, 637

PRIOR PELICATION DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SEQ ID NO 18161

PARCETAL PERIOR PELICATION NUMBER: PARCETAL PARCE
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                                                                                                                        17 GGGACCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGCGCTTTGGGAACCAGGCCG
                              211 TCTTCTTTCTTCGGCATGGACAGGCCCCTAAGCTGCGGGACGAGGATCTGATTCTGGCCC
                                                                                             CTGGCAGCCAGAGGTGCTCCGGGATTGCAAACTCCTCTTCTCACCTGCCAAAGATGGAGA
  1048 TCTTCTTCTTCGCCATGGACAGGCCCCCTAAGCTGCGGGACGACTTCTGATTCTGGCCG
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                                                                                                                                                                                                                                                                                                                                                                            GGTTCCTAGGAGCAGGACCATCTCCCATC 1316
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CORGANISM: DROSOPHILA
US-11-097-143-18161
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US-11-097-143-18161
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Best Local S:
Matches 563
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                                                                                                                                                                    915 GGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGA 974
                                                                                                                                                                                                                                                                                                                                                                                       190 CCAGGGGAGGCCGTCTTTTTTTTCGGCATGGACAGGCCCCCTAAGCTGCGGGACGAGTT
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                                                                                                        130 CCACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGAGCCT
                              1; Gaps
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29.1%; Score 441; DB 10; Length 479;
Best Local Similarity 98.9%; Pred. No. 4e-132;
Matches 444; Conservative 0; Mismatches 5; Indels
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US-09-918-95-19437
Sequence 19477, Application US/09918995
Publication No. US2003007362341
FUBLICATION NO. US2003007362341
FUBLICAMT: Hyeaq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PELLATON NUMBER: US/09/918,995
CURRENT PELLATION NUMBER: US/09/235,076
FRIOR APPLICATION NUMBER: US/09/235,076
FRIOR PILING DATE: 1999-01-20
NUMBER OF EQI ID NOS: 38054
SEQ ID NOS: 38054
SEQ ID NO 19377
98.1%; Pred. No. 1e-132;
tive 0; Mismatches 8; Indels
Best Local Similarity 98.19
Matches 458; Conservative
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; ORGANISM: Homo sapiens
US-09-918-995-19437
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Sequence 18160, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.

RESULT 14 US-11-097-143-18160/c

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Pred. No. 3.6e-37;
); Mismatches 476;
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUTITLE OF INVENTION: ARRAYS, FOR DETECTING ENTITLE OF INVENTION: DROSOPHILA GENES.

FITLE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR PELLORATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR PLILORATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-2
PRIOR PRILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-3
PRIOR FILING DATE: 2000-01-24
PRIOR PRILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR PRILING DATE: 2000-01-23
NUMBER OF SEQ ID NOS: 43008
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DETECTING
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Search completed: November 9, 2005, 15:51:13 Job time : 1357.3 secs
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US-09-783-590-11501
US-09-783-590-11501
Sequence 11501, Application US/09783590
Fatent No. US2002010850A1
Fatent No. US2002010850A1
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Fatent No. US20020110850A1
Fatent Normary Haseltine, William A.
APPLICANT: Haseltine, William A.
FAPPLICANT: Li, Hacdong A.
FAPPLICANT: Ruber, Steven M.
FILLS REPERENCE: PO-16.201
FILLS REPERENCE: PO-16.201
FILLS REPERENCE: PO-16.201
FILLS REPERENCE: PO-16.201
FATENT FILLNG DATE: 1995-04-12
FRIOR FILLNG DATE: 1995-04-12
FRIOR FILLNG DATE: 1994-11-21
625 CGG---CCCTATGTGGGCATTCATCTGGGCATTGGCTCTGACTGGAAGAACGCCTGTGCC 681
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                                                                                                                                                        1444 CACGICAAGGATAGCCAGCATCTGTTTGCCTCGCCGCAGTGCTTGGGGTATAAAATGAA 1385
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                                                                                                       682 ATGCTGAAGGACGG-----GACTGCAGGCTCGCACTTCATGGCCTCTCCGCAGTGT 732
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COTHER INFORMATION: n equals a,t,g, or c
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Best Local Similarity 83.9%; Pred. No. 5.7e-26;
Matches 177; Conservative 0; Mismatches 23;
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (301)
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November 9, 2005, 00:12:44; Search time 5490.13 Seconds (without alignments) 10496.888 Million cell updates/sec
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1 ATGCCGCGGGGCTCCTGGGA......TTTTGAAATCATTGAATTC 1514
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: gb estl:*
2: gb est2:*
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Database :

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	Description	CR617950	BX353274	AK081059	AK044629	BX345988	BQ677046	BM909055	BX345989	AL135434	BI524031	BX449172	BM475212	CO774833	BG747760	BP144264	BM972332	BQ964179	BI757540	BI410783	AW957639	BG473023	BQ936634	CN348925	BM711905
SUMMARIES	ID	CR617950	BX353274	AK081059	AK044629	BX345988	BQ677046	BM909055	BX345989	AL135434	BI524031	BX449172	BM475212	CO774833	BG747760	BP144264	BM972332	BQ964179	BI757540	BI410783	AW957639	BG473023	BQ936634	CN348925	BM711905
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ALIGNMENTS

CR617950 1555 bp mRNA linear HTC 21-JUL-2004 N full-length cDNA clone CS0DJ008YF12 of T cells (Jurkat cell line) N CR617950 CR617950.1 GI:50498757 HTC; CNSLT_cDNA. Home sapiens (human)		Genoscope. Jenoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequenc Submitted (20-JUL-2004) Genoscope - Centre National de Sequenc BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cn - Web : www.genoscope.cns.fr) Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and c into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Lib	was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 11555 /mol type="mRNA" /mol type="mRNA" /db xref="taxon:9606" /clone="CSODJO08YF12" /tissue type="T cells (Jurkat cell line) Cot /plasmid="pcMVSPORT_6"	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1445; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 1 CR617950 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL REMARK	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES source ORIGIN	Query Match Best Local Matches 144

1 ATGCCCGCGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGCGC 60

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AKO44629

Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930028F21 product:protein O-fucosyltransferase 1, full
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                  1025 AGCGGGACCTCCAGGGGAGGCCGTCTTCTTTCGGCATGGACAGGCCCCTAAGCTGC
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                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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     Encyclopedia Project of Genome Exploration Research Group in Ridenomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed the prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/.

URL: http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                    31; Gaps
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wattahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Haramoto, K., Hiramoto, K., Hiramoto, H., Hiramoto, K., Hiramoto, H., Kagawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Saico, H., Saato, R., Saico, H., Saato, H., Saato, R., Shinagawa, A., Shiraki, T., Saogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Murametsu, M., and Hayashizaki, Y., Tayamishi, A., Tayamishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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Submitted (16-JUL.)
Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enriched mouse cDNA library"
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the RIKEN Genome Exploration Research
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O-fucosyltransferase 1 (MGD|MGI:2153207, GB|NM_080463,
evidence: BLASTN, 99%, match=1290)
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/strain="C57BL/6J"
/db_xref="FANTOM DB:A930028F21"
/db_xref="taxon:10090"
/clone="A930028F21"
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/clone lib="RIKEN full-length/dev_stage="adult"
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/protein_id="BAC32009.1"
/db_xref="G1:26336653"
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6 (bases 1 to 2616)
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/translation="MGAAAWAPPHILIRASFILLILILPILPRGRSAGSWDLAGYLLYCP
CMGRFGWQADHFLGSLAFAKLIARTLAVPPWIEYQHKRPPFTNLHVSYQKYFKLEPLQ
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HVSFWKSELFTGISSFASYKEQWTQRFPAKEHPVLALPGARAQFPVLEHRELQKYWW
WSDEWVRTGEALISSHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYS
RSTAFPLTMFWCLPDLKEIQRAVTLWYRALNARSYYIATISSSYYSSIQQLFKDKRV
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AGENCOURT 8343300 NIH MGC_112 Homo sapiens cDNA clone IMAGE:6273476 BO677046
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 914)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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815 TGTGGGCATTCATCTGCGCATTGGCTCTGACTGGAAGAACGCCTGTGCCATGCTGAAGGA
                                                                                                        753 AGCGGCCCCCCCCACGATGACTATGTGCCTGCCTGACGAAGGAGATCCAGAGGGCTGT
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Homo sapiens

Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 889)

St. iv. W.B., Garuber.C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30375046.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Contact: Genoscope

Genoscope - Centre National de Sequencage

Contact: Genoscope

Genoscope - Centre National de Sequencage

List strand CDNA was primed with a Not! Olight prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecox V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster Por more information about this cluster, see

Por more information about this cluster, see

http://www.genoscope.cns.fr/cdna?e=CSOAJ008DCO6NPl&c=9980.f.

location/Qualifiers
                                         1140 GGAGCGGGACCTCCATGGGAGGCAGTCGTCTTTGGCATGGACGACCCTCCAGCT 1199
                                                                                                                                                                                                                                                                                                                                                                  BX345988 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED HOmo sapiens cDNA clone CSODJO08YF12 3-PRIME, mRNA sequence.

BX345988
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(cell_line="JURKAT"
(clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            footes "let strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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.larity 99.4%; Pred. No. 4.1e-227;
Conservative 2; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                          1083 GCGGGACGAGTTCTGGCCGGAGCACCAGACCTC 1122
                                                                                                                                                                                                                                                                      1200 TCGGGATGAATTTTGATCCCATCTGAAGCCCCCACCTCCC 1239
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ008YF12"
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10-NORMALIZED"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                          721 CAAAGCAGTCCCCCTCTTCTGGTCCACTCTCGAGCAGCAGCCTGGAAAGCTGAAA
                                                                                                                                                                                                                                                                                                       CTCTTCAGAGAGATTTTTTTATAGAGAGA-TTCTATAATTTTGATACAAGGTCATGACTA
661 GGAGCAGGAGCATCTCCCATCGCACGTGCTTTCTGCTCTTCTGGAATTTCTCACACTGG
                                                                                                                                                                                                                                                                             CTCTTCAGAGAGATTTTTTTTATAGAGATTTCTATAATTTTTGATACAAGGTCATGACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrabed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can betto: //image.lln.gov
Plate: LLCM1904 row: e column: 14
High quality sequence stop: 629.
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Pred. No. 7.4e-195;
); Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                            TCCTAGAACTCTCTGTGGTTTTTGAAA 1502
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                             GGAGCAGGAGCATCTCCCATCGCACGTGCT
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                 CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCA1453 row: h Column: 21
High quality sequence stop: 662.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BX345989
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 841)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                           GTGGCATACTGCTTTTGAGGTGGCAGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATG
                                                                                                    AAGGAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCG
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          AAGGAAGGAAACCCCCTTTGGCCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCG
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On May 5, 2003 this sequence version replaced gi:30377055. Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequencagencope.cns.fr, Web: www. genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mkNA"
/db_xref="taxon">clone="colonologyFl2"
/clone="ColonologyFl2"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
10-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Increasing strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR vietes of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 6.9e-188;
1; Mismatches 2;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5201616"
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BI524031.1 GI:15348823
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DKFZp76200115_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
DKFZp76200115_5', mRNA sequence.
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I bases 1 to 719)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin.
6, 14059
                                                                      1 GGAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAAGTGGA
               GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT
                                  GSCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT
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/lab_host="DH10B"
/clone_lib="762 (synonym: hmel2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No s1 sequence available.
This clone (DKFZp76200115) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 717.4; DB 1; Length 719;
Pred. No. 1.2e-187;
0; Mismatches 1; Indels 0
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKRZ276200115"
/tissue_type="melanoma (MeWo cell line)"
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/lab_host="DH10B"
/clone_llb="NIH MGC 122"
/noce="Organ: pooled lung and spleen; Vector: pCMV-SFORT6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
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603052202F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5201616 5',
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by Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (hases 1 to 1899)
1 (hases 1 to 1899)
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: Life Technologies, Inc.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   Plate: LLAM11505 row: d column: 01
   High quality sequence stop: 880.
   Location/Qualifiers
   I. .889
                                                                                  241 GGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGGCATTCATCTGCGCATTGGCTC
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BX449172.2 GI:47067286
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anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (Ecory site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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Query Match

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Matches 758, Conservative 0; Mismatches 78, Indels 4,
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BX449172 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODMO14YKI1 5-PRIME, mRNA sequence.

LOCUS DEFINITION

ACCESSION

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The floates I to 889 in the sequence oversion replaced gi:31030014.

Li W.B., Gruber C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On May 22, 2003 this sequence version replaced gi:31030014.

Contact: Genoscope
Contact: Genoscope
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequence Genoscope.cns.fr, Web: www.genoscope.cns.fr

Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCNVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 9980.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOAM014AF06GP1&c=9880.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
//organism="Homo sapiens"
//db xref="taxon:9606"
/clone="CSODMO14YK11"
//tissue_Yrpe="FETAL LIVER"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BCORV sites of the pCMVSPORT 6 vector: Library was not normalized."
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                                                            Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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                                                         Eukaryota, Metazoa, Chordata,
Mammalia, Butheria, Primates,
1 (bases 1 to 898)
sapiens (human)
sapiens
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Sequenced on 2004.07.21. 611 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca nemestrina
Macaca nemestrina
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                              123 TGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACC
                                                                                                                                                                           GATTCTGGCCGGAGCACCACCGACCTCTGATCCTGGAGGACCAGAGTCTGAGCTGCTCCT
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                        CTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAGG
                                                                                                  TGGTGAGCCTGAAGCCTGAGGTGGCCCAAGGTCGACCTGTACATCCTCGGCCAAGCCGACC
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IBIUW:29960 57 similar to Bases 7 to 852 highly similar to P
POFUT1 (Hs.178292), mRNA sequence.
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(Carcopithedrae; Macaca.

(Carce, M.G. Thomas, M., Korth, M., Iadonato, S.P. & Large-scale Rhesus Macaque cDNA Sequencing (Unpublished (2003)
(Contact: C. Magness

11) uniquen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98136
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5', mRNA sequence.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clome=IMAGE:559347"
/tissue type="duodenal adenocarcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/clone_lib="NHH MGC 88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_l: NotL; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12283 row: m column: 12
High quality sequence stop: 685.
CTTTTTACAGGCATTTCCTTCAGTGCTTCGTACAGAGAACAATGGAGCCAGAGATTTTCT
                                                      TGACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGC
                                    CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGCCCCAGCCCAGTTCCCCGGTCCTAGAA
                                                                                                              GAACACACACTACAGAAGTACATGGTATGGTCAGACG-AAATGGTGAAGACGGGAGA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 704)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 2.7e-178;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BM475212.1 GI:18524254
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ilarity 99.7%;
Conservative
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 808)

NIH-WGC http://mgc.nci.nih.gov/.

NIH-WGC http://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (WGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium(LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI675 row: n column: 14

High quality sequence stop: 808.

Location/Qualifiers

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//cranigm-Hrmc caniaca.
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602705255F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842061 5',
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Homo sapiens
                                                                                                     777 GIGCCIGCCI 786
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BG747760
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AUTHORS
TITLE
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COMMENT
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                                                                                                                                                                                                                                                                          /lab_host="Electromax DH10B"
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/clone lib="Katze NNLV"
/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
/site_2: BsrG I; Created from CloneMiner cDNA_Library
ConsEruction kit (catalog #18249-029)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCCAGTTCCCCGTCCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Local Similarity 94.1%; Pred. No. 2.6e-175;
les 743; Conservative 0; Mismatches 43; Indels 4
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/strain="Indian"
/db xref="taxon:9545"
/clone="IBIUW:29960"
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BACKWARD: CACTACTPAAGGGGACAATGGGTA
INSERT LENGTH: 942 Std Error: 0.00
Plate: CL000531 row: E column: 09
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYANNO.
                                                                                                                                 Location/Qualifiers
1. .942
     http://www.macaque.org
                                                                                                                                                                                                                                                              /sex="male"
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1. .801
| /organism="Sus scrofa"
| /organism="Sus scrofa"
| /organism="Sus scrofa"
| /db _ xref="taxon: 9823"
| /clone="OVR010034G09"
| /tissue_type="ovary"
| /dev_stage="adult"
| /clone_lib="full-length enriched swine cDNA library, adult ovary"
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     on the quality values.
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                                                                                                                                                                                                                43.6%; Score 660.2; DB 5; Length 89.0%; Pred. No. 1e-171; ive 0; Mismatches 88; Indels
 ty bases were trimmed based Location/Qualifiers
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1 (Joases I to 801)

Suchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

Nucleic Acida Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-818-8627

Email: huenishi@affrc.go.jp

EST project With full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP144264 BP144264 Eull-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVR010034G09 5', mRNA sequence.
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                                                                                                                            GCATACTGCTTTGAGGTGGCAGCCAGGAAGCCCAGATAAGAAGACGTGCCCCATGAAG
                    CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTAC
                                                                                  GCATACTGCTTTTGAGGTGGCAGCCCAGCGAAGCCCAGGTAAGAAGACGTGCCCCATGAAG
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                                                               AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG
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BP144264
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360 613 420 673 480 733 540 793 900 853 999

TITLE

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720 973

Search completed: November 9, 2005, 10:38:05 Job time: 5495.13 secs

AF375885 MUS mUSCU BC046259 MUS mUSCU A734581 BOS tauru A7320352 Gallus ga BC082519 Xenopus t A7720352 Gallus ga BC082519 Xenopus t A781425 Xenopus 1 A781504 Tetraodon A781505 Danio rer BC000582 Homo sapi A71121897 Human DNA AK112708 Ciona int AK124093 Homo sapi AC094844 Rattus no AC094844 Rattus no AC09481371 Rattus no AC078911 MUS mUSCU A181502 Ciona sav A781502 Ciona sav

Scoring table:

Minimum DB Maximum DB

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TITGGGAACCAGGCCGATCACTICTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT
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Wang, Y. and Spellman, M.W.
O-fucosyltransferase
Patent: US 6270987-A 16 07-AUG-2001;
Location/Qualifiers
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AR163457.1 GI:16234062
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Matches 1100; Conservative
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AR164451 Sequence
BD103188 O-fucosyl
AR163452 Sequence
BD103189 O-fucosyl
AR35984 Homo sapin
BD103190 O-fucosyl
BD103190 O-fucosyl
BD103191 O-fucosyl
AR781500 Pan trogl
AR163453 Sequence
AL832023 Homo sapin
AR163453 Sequence
BD103191 O-fucosyl
AR34580 Bos tauru
AR341503 Bos tauru
AR3679917 Sus scroft
AR3679917 Sus scroft
AR36199 Rattus no
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10740.434 Million cell updates/sec
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1 ATGCCCGCGGGGCTCCTGGGA......CTGCGGGACGAGTTCTGATT 1100
                    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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AR163453 BD103191 AY344580 AJ781503 SSC567917 AJ781499

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Qy 301 GCATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360 Db 301 GCATACTGCTTTGAGGTGGCAGCCAGCGAGATAAGAAGACGTGCCCCATGAAG 360 Qy 361 GAAGGAACCCCTTTGGCCCATTCTGGGATTTCATGTGAGTTTCAACAAGTCGGAG 420 Db 361 GAAGGAAACCCCTTTGGCCATTCTGGGATCAGTTTCAACAAGTCGGAG 420 Db 361 GAAGGAAACCCCTTTTGGCCCATTCTGGGATCAGTTTCAACAAGTTCCAACAAGTTCCAACAAGTTCCAACAAGTTTCAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAAAA	Qy 421 CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT 480 Db 421 CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAACAATGGAGCCAGAGATTTTCT 480 Qy 481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGCCCCAGCCCAGTCCCGTCGTAGAA 540				JOURNAL Patent: JP 2001527389-A 1 25-DEC-2001; GENENTECH INC COMMENT OS Unidentified
Qy 721 TCTCCGCAGTGTGTGGGCTACAGCCGCAGCACAGCCCCCCCTCACGATGACTATGTGC 780 Db 721 TCTCCGCAGTGTGTGGGCTACAGCCACAGCACACCCCCCCC	Qy 841 CAGTCGGTCTACGTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900 bb		Qy 1021 CGGGAGCGGAGCCTCCAGGGGAGGCCGTCTTCTTCTTCGGCATGGACAGGCCCCTAAG 1080 Db 1021 CGGGAGCGGCACCTCCAGGGAGGCCGTCTTCTTTCTTCGGCATGGACAGGCCCCTAAG 1080 Qy 1081 CTGCGGAACTCTGATT 1100 Db 1081 CTGCGGAACTCTGATT 1100	ARIESULT 3	

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CTCGGCCAAGCCGACCACTTTAITCGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020
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TCTCCGCAGTGTGTGGGCTACAGCCGCACACAGCGGCCCCCCTCACGATGACTATGTGC 780
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                                               CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTGAGGTGGGTTG
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Pred. No. 2.4e-253;
0; Mismatches 1; Indels 0;
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Unclassified.

E 1 (bases 1 to 1300)
S Wang, Y. and Spellman, M.W.
O-fucosyltransferase
AL Patent: US 6270897-A 6 07-AUG-2001;
Location/Qualifiers
1007-1300
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Sequence 6 from patent US 6270987.
AR163452 GI:16234057
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Matches 1099; Conservative (
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             25-DEC-2001
17-DEC-1997 JP 1998532877
31-JMN-1997 US 08/792498,26-NOV-1997 US WANG,MICHAEL W SPELLMAN
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
                                                                                                                            Location/Qualifiers
1. 1514
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Location/Qualifiers
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17-DEC-1997 JP 1998532877

13-JAN-1997 US 08/792498,26-NOV-1997

WANG,MICHAEL W SPELLMAN

C12N15/54,C12N9/10,C07K16/40

Strandedness: Single;

Topology: Linear;

O-fucosyltransferase

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Pred. No. 2.4e-253;
0; Mismatches 1;
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1 (bases 1 to 1300)
Wang, Y. and Spellman, M.W.
O-fucosyltransferase
Patent: JP 2001527389-A 2 25-DEC-2001;
GENENTECH INC
OS Unidentified
PN JP 2001527389-A/2
PD 25-DEC-2001
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BD103189.1 GI:22648763
JP 2001527389-A/2.
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GNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLHVSYQKYFKLEPLQÀYHRV ISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFRUOFHYSFN KSELFTGISFGASYREQWSQRFSPKEHPVLALGGAPAQFPVLEEHRPLGKYWWSDEM VKTGEAQIHAHLVRPYVGTHLRIGSDWKNACAMLKOGTAGSHFMASPQCVGYSKSTAA PLTWTMCLPDLKEIQRAVKIWVRSLDAQSVYVATDSESYYPELQGLFKGKVKVVSLKP EVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLRDEF"	Query Match 99.9%; Score 1098.4; DB 9; Length 5249; Best Local Similarity 99.9%; Pred. No. 2.4e-253; Matches 1099; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 1 ATGCCGGGGGCTCCTGGGCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGCGC 60	Qy 61 TITIGGGAACCAGGCCGATCACTTCTGGGCTCTCTGGCAATGCTGCTAAACCGT 120	Oy 121 ACCTTGGCTGTCCCTTGGATTGAGTACCAGGATCACAAGCCTCCTTTCACCAACCTC 180	181	Db 359 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCCCCCCC	Qy 301 GCATACTGCTTTGAGGTGGCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360	Qy 361 GAAGGAAACCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGAG 420	QY 421 CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTCT 480 DD 539 CTTTTTACAGGCATTTCCTTCAGTGCTTCCTTCAGAGAACAATGGAGACCAGAGATTTTCT 598	Qy 481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGGCCCCAGCCCAGTTCCCCGTCCTAGAA 540	Oy 541 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGAAGAATGGTGAAGAAGGAGGAGG 600 nh 659 GAACAAGGCCACTACAGAAGTACATGGTATGGTCAGAAGAATGGTGAAGACGGGAAGA 718	601	72 83	721	QY 781 CTGCCTGAACGAGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840 Db 899 CTGCCTGAACGAGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 958	Qy 841 CAGTCGGTCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900	901 AAAGGAAAGGTGAAGGTGAAGCTGAAGCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 960
Qy 781 CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGGTCTGGGTGAGGTCGCTGGATGCC 840 Db 916 CTGCCTGACTGAAGGAGTCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGTGGATGCC 975 Qy 841 CAGTCGTCTACTTGATTCCGAGAGTTATGTGCTGAGCTCCAACAGCTCTTC 900 Db 976 CAGTCGGTCTACCTACTTCCTAATTCCGAAGATTATGTGCCTCAACAGCTCTTC 111111111111111111111111111111111111	901	QY 961 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020	QY 1021 CGGGAGCGGAACTCCAGGGAAGCCGTCTTCTTCTTCGCATGGACAGGCCCCCTAAG 1080 Db 1156 CGGGAGCGGGACCTCCAGGGAAGCCGTCTTCTTCTTCGCATGGACAGGCCCCTAAG 1215	Qy 1081 CTGCGGGACGACTTCTGATT 1100 	AF375884 523-OCT-2	Homo sapiens protein o-fucosyltransferase cds. AF375884	VERSION AF375884.1 GI:15825113 KEYWORDS . SOURCE Homo sapiens (human) ORGANISM Homo saniens		and Haltiwanger, R.S. TITLE Modification of epidermal growth factor-like repeats with O-fucose. Molecular cloning and expression of a novel GDP-fucose protein O-fucosyltransferase	JOURNAL J. Biol. Chem. 276 (43), 40338-40345 (2001) MEDLINE 21523965 PUBMED 11524432 REFERENCE 2 (bases 1 to 5249)	Shi,S., Stanley,P., Wang,Y., Shao,L., Harris,R.J., St and Haltiwanger,R.S. Direct Submission	Medicine, 1300 Morris Park Ave., New York, NY 10461, USA Location/Qualifiers ce 1. :5249	/organisms="HQmo saplens" /mol_type="mRNA" /db_xref="taxon:9606" /db_tronosome="20" /man="hotween plag12 and KTP1R"	/tissue_type="heart" gene 1.5249 /gene="poFUTI" CDS 501216	<pre>/gene="POFUT1" /function="catalyzes transfer of fucose from GDP-fucose to serine or threonine on epidermal growth factor-like repeats"</pre>	<pre>/note="0-FucT-1; glycosyltransferase" /codon_start=1 /product=#protein o-fucosyltransferase" /product=#protein o-fucosyltransferase"</pre>	/procein_re="Adloys". /db_xref="G1:1585114" /translation="MGAAAWARPLSVSFLLLLLPLPGMPAGSWDPAGYLLYCPCMGRF

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	RESULT 8 BD103190	Location/Qualifiers	Oy 61 TTTGGGAACCAGGCGATCACTTCTTGGGCATTTGCAAAGCTGTAAACCGT 120 RE Db 4296 TTTGGGAACCAGGCTCTTGTGGCATTTGCAAAGCTGCTAAACCGT 4355 LC Db 121 ACCTTGGCTGTCCTTCTTGGATTGAGTACCAGCATCACAAGCTTCACCAACCTC 180 AC Oy 121 ACCTTGGCTGTCCTTGGATTGAGTACCAGCATCACAAGCTTCACCAACCTC 4415 VW VD 4356 ACCTTGGCTGTCCTTGGATTGAGTACCAGCATCACAAGCTTCACCAACCTC 4415 KB Oy 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGACCCCTCCAGGCTTACCATCGATCATC 240 KB Oy 181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGACCCTCCAGGCTTACCATCGATCATC 4475 RE Oy 241 AGCTTGGAGGAATTTCAAGCTGGCCCCTCCAGGCTTACCATCGGGTCATC 4475 RE Oy 221 AGCTTGGAGGATTTCATGGAGCCCCTCCAGGCTTACCATCGGGTCATC 4475 RE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Ohara,O., NagaseFT., Kikuno,R. and Nomura,N.
Direct Submission
Submitted (12-DEC-1995) Osamu Ohara, Kazusa DNA Research Institute;
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdhainfo@kazusa.or.ip, Tel:+81-438-52-3913)
On May 9, 2002 this sequence version replaced gi:1136419.
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The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-1 bNA Res. 3 (1), 17-24 (1996)
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                                                                                                         Chiang, P.W., Wang, S., Smithivas, P., Song, W.J., Ramamoorthy, S., Hallman, J., Puett, S., Van Keuren, M.L., Cromber, E., Kumar, A., Glover, T.W., Miller, D.E., Tsai, C.H., Blackburn, C.C., Chen, X.N., Sun, Z., Cheng, J.F., Korenberg, J.R. and Kurnit, D.M. Cheng, J.F., Korenberg, J.R. and Kurnit, D.M. Chantification and analysis of the human and murine putative chomics 34 (3), 328-333 (1996)
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0; Mismatches 2; Indels 0;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority
humanexons or transcripts, for detecting expression and c
                                                                                                                                                                                6; Length 1167;
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Pred. No. 7.3e-253;
0; Mismatches 1;
                                                                 Patent: WO 02068579-A 13711 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 1167
/ organism="Homo sapiens"
/ mol_type="unassigned DNA"
/ db_xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae,
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Best Local Similarity 99.7%; Pred. No. 1.4e-25.2
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1 (bases 1 to 4560)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo.G., Ham,M. and Wiemann,S.

Direct Submission
Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
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                                                                                                                    GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCTAACAAGTGG
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                                              GCATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCCAGATAAGAAGACGTGCCCCATGAAG
                                                                                                GAAGGAAACCCCTTTGGCCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG
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Homo sapiens mRNA; cDNA DKFZp451J114 (from
AL832023
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Homo sapiens
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Martinez-Duncker, I., Mollicone, R., Candelier, J.J., Breton, C.
Oriol, R.
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Submitted (06-JUL-2004) Oriol R.,
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
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Pan troglodytes (chimpanzee)
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/product="protein-O-fucosyltransferase
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966 CCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTGTGAAGCGGGGA 1025
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781 GGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAACG G10
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GGAACATCCGGTGCCTTGCCCTGCCAGGAGCCCCAGGCCCCAGTTCCCCGTCCTAGAGGAACA
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unidentified
unclassified.
1 (Dases I to 5009)
Wang, Y. and Spellman, M.W.
O-fucosyltransferase
Patent: JP 2001527389-A 4 25-DEC-2001;
GENEWATCH INC
OS Unidentified
PN JP 2001527389-A/4
PD 25-DEC-2001
PF 31-JAN-1997 US 08/792498, 26-NOV-1
PR STANDEDGES: Single;
CC TOppology: Linear;
CC Toppology: Linear;
CC O-fucosyltransferase
CC Toppology: Linear;
CC O-fucosyltransferase
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CAGTCGGTCTATGTTGCTACTAATTCCGAAGTTATGTGCCTGAGGCTCCAACAGCTCTTC 969
                                                                        AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 960
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AR163453 GI:16234058
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15009 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"	93.94; Score 1033.4; DB 6; Length 5009; arity 99.9%; Pred. No. 1e-237; onservative 0; Mismatches 1; Indels 0; Gaps 0;	125 60 185		GENERAL CARCAGARGIACITICARGETIGGAGETICACATEGGGETATEGGGTT 180 GGAGGATITICATGGAGAGAGAGCCCCCCCCCTGAGAAGCGGGTGGCATA 305	CTGCTTTGAGGTGGCAGCCCAGAAGCCCAGATAAGAAGACGTGCCCCATGAAGGAAG	AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTT 425	TACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGGATTTTCTCCAAA 485 	GGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGTTCCCCGTCCTAGAAGAACA 545	CAGGCCACTACAGAAGTACATGGTAGGACGAAATGGTGAAGACGGGAGAGGCCCA 605	GATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCTGACTG 665	GAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGCTCGCACTTCATGGCCTCTCC 725		TGACCTGAAGGAGTCCAGAGGCTGTGAAGCTCTGGGTGGG	GGTCTACGTIGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGG 905	GAAGGTGAAGGTGAGGCTGAAGCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGG 965	CAAGCCGACCACTTTATTGGCAACTGFGTCTCCTCTTCACGCTTTGTGAAGCGGGA 1025
o	y Match Local Similarit hes 1034; Conse	66 GAA(1 GAA(126 GGC		246 GGAC 181 GGAC	306 CTGC 241 CTGC	366 AAAC 301 AAAC	426 TACA 361 TACA	486 GGAA 421 GGAA	546 CAGO 481 CAGO	606 GATT 	666 GAAG 601 GAAG	726 GCAG 661 GCAG	786 TGAC 721 TGAC	846 GGTC 781 GGTC	906 GAAC 841 GAAC	966 CCAP 901 CCAP
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Aak79915 Human imm
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Abl13946 Drosophil
Abl13894 Human sec
Abl44539 Human sigl
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Aad07629 Human sec
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Adf81754 Leukaemia
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1 ATGCCCGCGGGCTCCTGGGA......CTGCGGGACGAGTTCTGATT 1100
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Aah52044 Mycobacte	AAH52044	4	2370	3.4	37.8	45	
Adt41577 Bacterial	ADT41577	13	1234	3.4	-	44	υ
Ads63974 Bacterial	ADS63974	13	1234	3.4	37.8	43	υ
Ads63598 Bacterial	ADS63598	13	1234	3.4	37.8	4	υ
Aca64963 Human cor	ACA64963	œ	6227	3.5	38.4	41	
Abt10150 Human bre	ABT10150	9	6227	3.5	38.4	40	
Ach26305 Human adu	ACH26305	σ	532	3.5	38.4	39	
Ade25660 Human cDN	ADE25660	2	2670	3.5	38.6	38	
Ade77025 Human cDN	ADE77025	12	2358	3.5	œ.	37	
Adi62782 Human apo	ADI62782	10	1596	3.5	38.6	36	
Abx46567 Bovine ES	ABX46567	8	407	3.5	38.6	35	
Abd01484 Pseudomon	ABD01484	11	1353	3.5	39	34	
Abd01472 Pseudomon	ABD01472	11	1131	3.5	39	33	
Aca43606 Prokaryot	ACA43606	œ	372	3.5	39	32	
Ada69815 Rice gene	ADA69815	œ	1554	3.6	40	31	
Aav65635 Northern	AAV65635	~	40	3.6	40	30	
Aav65637 Primer am	AAV65637	7	40	3.6	40	53	
Adb75488 Prostate	ADB75488	10	5932	3.7	40.4	28	
Adq84111 Human tum	ADQ84111	12	5704	3.7	40.4	27	
Adq80232 Brain-spe	ADQ80232	13	5019	3.7	40.4	56	
Aah97782 Murine 7-	AAH97782	S	558	3.7	40.6	N	U
Aad08215 Human gen	AAD08215	4	114793	3.7	41.2	24	O
Aca31561 Prokaryot	ACA31561	8	1438	3.9	42.4	23	
Ada71938 Rice gene	ADA71938	œ	2000	4.2	46.2	22	U
Ada71938 Rice gene	ADA71938	œ	2000	4.5	5.0	21	

ALIGNMENTS

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Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                           O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                                                                                             Location/Qualifiers
1. .1100
/*tag= b
/note= "this actively expressed O-fucosyltransferase agenone is claimed for in claim 9"
                                                                                                                                                                                                                        heart O-fucosyltransferase"
                                                                        Human heart O-fucosyltransferase encoding DNA.
                                                                                                                                                                                                             /*tag= a
/product= "human
          AAV65632 standard; DNA; 1514 BP.
                                                                                                                                                                                                                                                                                     97WO-US023401
                                                                                                                                                                                                                                                                                                         97US-00792498.
                                                   16-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                            Spellman MW;
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-437477/37.
P-PSDB; AAW80571.
                                                                                                                                                                                                                                                                                     17-DEC-1997;
                                                                                                                                                                                                                                                                                                         31-JAN-1997;
26-NOV-1997;
                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                             WO9833924-A1
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                06-AUG-1998
                               AAV65632;
                                                                                                                                                                                                                                                                                                                                                            Wang Y,
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This represents the nucleotide sequence of the plasmid construct used for the expression of human heart O-fucosyltransferase. The human O-fucosyltransferase and place an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of
CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermal growth factor diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4140. .5333
/*tag= a
4218. .4.335
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O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                             CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid construct for expression of human O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human O-fucosyl:transferase able to glycosylate domains - useful for diagnosis and treatment of overexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4218. .4235
/*tag= b
/note= "polyhistidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 49-57; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCGGGACGAGTTCTGATT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spellman MW;
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P-PSDB; AAW80573.
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Synthetic.
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26-NOV-1997;
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                                                                     This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EPP) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to probe associated with overexpression of D-fucosyltransferase, to prope associated with overexpression of Probes based on EPF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                             Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
                            Fig 12A; 90pp; English
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                            Claim 9;
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O-fucosyltransferase, e.g. mutants with increased affinity for the EPG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
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CITITITACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT
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Pred. No. 1.3e-305;
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                 5136 AAAGGGAAGGTGAAGGTGGAGCCTGAAGCCTGAGGTGGCCCCAGGTCGACCTGTACATC
                                                                 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG
AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCCCAGGTCGACCTGTACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target, TAT; human, overexpression; continuour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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Claim 1; SEQ ID NO 5725; 7273pp; English.

The invention relates to human tumour-associated antigenic target. (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acids and antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with

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1 ATGCCCGCGGGCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC
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increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, luyer cancer, bladder cancer, parcreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
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Best Local Similarity 99.8%; Pred. No. 2.7e-305;
Matches 1098; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 99.7%; Pred. No. 5.2e-305;
Matches 1097; Conservative 0; Mismatches 3; Indels 0; C
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The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
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R, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, in diagnosis and gene therapy.
                                                                                                                                                                                                                                                               Human, cytokine, cell proliferation, cell differentiation, gene th vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomodulatory, cancer, leukaemia, nervous system disorder; arthiritis, inflammation, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
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Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
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BP.
                                                                                                                                                                                                   Human polynucleotide SEQ ID NO
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27-AFR-2000; 2000US-00560875.
29-UJN-2000; 2000US-00590075.
19-UJL-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
AAK51510 standard; cDNA; 5230
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                                                                                                                                 (first entry)
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P-PSDB; AAM78377.
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Matches 1048; Conserv
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Ma Y, Zhao QA, W
Xue AJ, Yang Y,
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(first entry)

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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomedulatory; cancer, leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                   Human polynucleotide SEQ ID NO 2023.
                                                                                                                                                                          03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-UUN-2000; 2000US-00590075.
19-UUJ-2000; 2000US-0063936.
15-SEP-2000; 2000US-00654936.
20-OCT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                           05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                      WO200157190-A2.
                                                                                                      Homo sapiens.
                   06-NOV-2001
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AAK52494;
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                                                                                                              AGAAGCGGGTGGCATACTGCTTTGAGGTGGCAGCCCAGAAGCCCAGATAAGAAGACGT 349
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            TGCTAAACCGTACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCAAGCCTCCTT
                                                                                     CCGTCCTAGAGGAACACAGGCCACTACAGAAGTACATGGTTAGGTCAGACGAAATGGTGA
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 TGCTAAACCGTACCTTGGCTGTCCCTTCGTTGGATTGAGTACCAGCATCACAAGCCTCCTT
                                                 TCACCAACCTCCATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACC
                                                                                                                         GCCCCATGAAGGAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCA
                                     TCACCAACCTCCATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACC
                                                                          ATCGGGTCATCAGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACTGGCCCCTG
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to erytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity is the cell and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 211 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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   Y;
Wang
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94.7%; Score 1041.4; DB 4; Length 4850;
Best Local Similarity 99.4%; Pred. No. 2.5e-289;
Matches 1045; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4850 BP; 1142 A; 1218 C; 1244 G; 1246 T; 0 U; 0 Other;
   Xu C,
Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4424-4425; 6221pp; English.
                                                                                                                                             2001-476283/51.
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AAK52494 standard; cDNA; 4850

RESULT 6
AAK52494
ID AAK5

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This represents a first EcoR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial cDNA encodes for a protein of unknown function from myeblast cell line KG-1. The invention provides a human heart of fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated o-fucose residue. Inhibitors of o-fucosyltransferase, eg. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTT
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O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1033.4; DB 2; Length 5009;
Pred. No. 5.1e-287;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5009 BP; 1235 A; 1195 C; 1268 G; 1311 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 11; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.9%;
                                                                                                                                                                                                                    97US-00792498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overexpression of the enzyme
                                                                                                                                                                          97WO-US023401
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Matches 1034; Conservative
                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
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                                         Homo sapiens
                                                                                                                                                                       17-DEC-1997;
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26-NOV-1997;
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O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;

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616 CACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCTGACTGGAGAAGAAGCGC 675
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                                                                                                                                                                                       29-OCT-1999; 99US-0162237P.
21-JUL-2000; 2000US-0219666P.
                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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P-PSDB; AAE03110.
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                                                                             GATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCTGACTG 665
                                                                                                                                  GAAGAACGCCTGTGCCATGCTGAAGGACGGACTGCAGGCTCGCACTTCATGGCCTCTCC 660
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                                                                                                                     GAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCCTCTCC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; treumatoid atthritis; inflammation; allegy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepais; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastroinestinal disorder; programcy-related disorder; gentlerosis; complexinal disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; chromosome 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein-encoding gene 18 cDNA clone HMWEY26, SEQ ID NO:69
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/product= "Human secreted protein precursor"
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protein genes, and AAE03052-AAE03126 represent the proteins they encode.

AAE03127-AAE03150 represent human secreted protein fragments. The genes

AAE03127-AAE03150 represent human secreted protein fragments. The genes

and their corresponding secreted proteins are useful for preventing,

treating or amelicating medical conditions, e.g., by protein or gene

therapy. Pathological conditions can be diagnosed by determining the

cumunt of the new protein in a sample or by determining the presence of

mutations in the new genes. Specific uses are described for each of the

cumulations in the new genes. Specific uses are described for each of the

mutations in the new genes. Specific uses are described for each of the

cumulations in the new genes. Specific uses are described for each of the

mutations in the new genes. Specific uses are described for each of the

cumulations in the new genes. Specific uses are described for each of the

mutations in the new genes. Specific uses are described for each of the

cumulations in the new genes. Specific and evalonmental

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and include developing products for the diagnosis or treatment of

collections and developmental

collections and developmental

disorders, heamatopoletic disorders, disease of the immune services in all collibration, to prevent skin sping due to sunburn, to

maintain organs before transplantation, for supporting cell culture of

prinary tissues, to regenerate tissues, to identify their cognite ligands

correctly parameters, and in chemctaxis, and can be used to binding partners, and in chemctaxis, and can be used as a food

additive or preservative to modify storage properties of prinary tissues, to regenerate tissues, to identify their cognite ligands

correctly parameters, and in chemctaxis, and can be used in alleviating

symptoms associated with the disorders mentioned above, and in diagnostic

conditive or presert sequence represents a human secreted protein-

conditions and the 
/transl_except= (pos:4. .6, aa:Xaa)
/transl_except= (pos:10. .12, aa:Xaa)
/transl_except= (pos:13. .15, aa:Xaa)
/transl_except= (pos:442. .444, aa:Xaa)
/note= "Xaa equals any of the naturally occurring L-amino acids; CDS dees not include start codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels 0;
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43.0%; Score 473.4; DB 4; Length 915;
Best Local Similarity 98.4%; Pred. No. 8.7e-126;
Matches 477; Conservative 1; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 915 BP; 209 A; 253 C; 247 G; 202 T; 0 U; 4 Other;
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/*tag= b
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/*tag= c
/product= "Mature human secreted protein"
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1; SEQ ID NO 8126; 41pp; English ..

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436 CAGGGGGAGSCCGTCTTTCTTCGGCATGGACAGGCCCCCTAAGCTGCGGGACGACTTC
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environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                      TGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCCTCT
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine mucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention ms therefore useful for assessing the toxicity assays. The invention is therefore useful for assessing the conjugated including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that conducing electronic Northerns that allow the user to determine the cell producing electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expression level of a given gene in a particular tissue or cell. The methods are useful for predicting at least one toxic response or the compounds. The methods are useful for predicting at least one toxic response or the toxic response or the liver (liver necrosis, fatty liver likelihood that a compound or test agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver conjesses, protein adduct formation or hepatitis), those of the kidney, hard the toxins. The methods are also useful for predicting or elucidating compound or test agent will induced or modulated by the compound or test agent will now a known coxin. The present sequence is compound or test agent also useful for predicting or elucidating compound or test agent which was claimed for use during the methods are also useful for predicting or elucidating compound or test agent due to the similarity of the expression profile induced by a known coxin. The present sequence is
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Pred. No. 1.8e-106;
0; Mismatches 54; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 610 BP; 155 A; 171 C; 149 G; 129 T; 0 U; 6 Other;
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89.0%;
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Matches 446; Conservative
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12-SEP-2000; 2000US-0231958P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232399P.
14-SEP-2000; 2000US-02324997P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-023493P.
12-SEP-2000; 2000US-023493P.
12-SEP-2000; 2000US-023493P.
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14-SEP-2000; 2000US-023493P.
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16-NOV-2000; 2000US-0246474P.
16-NOV-2000; 2000US-0246474P.
16-NOV-2000; 2000US-0246474P.
17-NOV-2000; 2000US-024622P.
17-NOV-2000; 2000US-024621P.
17-NOV-2000; 2000US-024921P.

    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34727
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                    Human reproductive system related antigen DNA SEQ ID NO: 6032
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2000US-0220963P.
2000US-0220964P.
2000US-0224518P.
2000US-0224519P.
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2000US-0225214P.
2000US-022526FP.
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2000US-0214886P.
2000US-0215135P.
2000US-0216647P.
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2000US-0217487P.
2000US-0217496P.
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                                 (first entry)
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                                                                                                                                                            Homo sapiens.
                                 21-NOV-2001
                                                                                                                                                                                                                                 02-AUG-2001
AAL03344;
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cxpression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I), Additionally, (I)
protein any be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antign genomic
sequences from the present invention. AAK6992 to AAK6950 and AAM82169
represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                   Ruben SM;
       05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025198BP.
06-DEC-2000; 2000US-025149P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-025186BP.
08-DEC-2000; 2000US-025186BP.
08-DEC-2000; 2000US-025186BP.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
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2000US-0232400P

14-SEP-2000;

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PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-02330663P.
PR 14-SEP-2000; 2000US-02330663P.
PR 21-SEP-2000; 2000US-02330665P.
PR 21-SEP-2000; 2000US-02330665P.
PR 22-SEP-2000; 2000US-023423P.
PR 22-SEP-2000; 2000US-023499P.
PR 22-CCT-2000; 2000US-02349P.
PR 22-CCT-2000; 2000US-02349P.
PR 22-CCT-2000; 2000US-02349P.
PR 22-CCT-2000; 2000US-02349P.
PR 22-CCT-2000; 2000US-023419P.
PR 22-CCT-2000; 2000US-0244617P.
PR 22-CCT-2000; 2000US-0244617P.
PR 22-CCT-2000; 2000US-024617P.
PR 22-CCT-2000; 2000US-0249211P.
PR 22-CCT-2000; 2000US-0249211P.
PR 22-CCT-2000; 2000US-024921P.
PR 22-CCT-2000; 2000US-024921P.
PR 22-CCT-2000; 2000US-0249291P.
PR 22-CCT-2000;
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716 TGGCCTCTCCGCAGTGTGGGCTACAGCCGCAGCACCACGCCCCCCTCACGATGACTA 775
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                                                                                                                                                                                        Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                         656 GCTCTGACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGCTCGCACTTCA
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.8%; Score 251.2; DB 4; Length 10331; Best Local Similarity 97.0%; Pred. No. 3.4e-61; Matches 256; Conservative 0; Mismatches 8; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                       Sequence 10331 BP; 2718 A; 2405 C; 2599 G; 2609 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6032; 1297pp + Sequence Listing; English.
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                                                                                                                                     Rosen CA, Barash SC, Ruben SM
08-DEC-2000; 2000US-0251856P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251989P.

08-DEC-2000; 2000US-0251989P.

11-DEC-2000; 2000US-0251990P.

11-DEC-2000; 2000US-02596P.
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ID ACH32225 standard; cDNA; 479
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                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                WPI; 2001-465570/50.
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                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide corresponsible for genetic disorders and other traits. The nucleotide correct or chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/RST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. The sequence contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGAGCGGGACCTCCAGGGGAGGCCG 1047
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                                                                                                                                                               New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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genome mapping; biodiversity; genetic disorder.
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                                                                                                              Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 479 BP; 99 A; 140 C; 143 G; 97 T; 0 U; 0 Other;
                                                                                                             Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.2%; Score 233; DB 9; L
100.0%; Pred. No. 1.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. ...
                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 19437; 44pp; English.
                                                                                                             Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human endothelial cell cDNA #3665.
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30-JUL-2001; 2001US-00918995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 233; Conservative
                                                       STACHE-CRAIN B.
                                                                                                             Labat I,
                                                                                                                                                                                                          antisense DNA or RNA.
                           DRMANAC R T.
                                                                  JONES L W.
                                                                                                                                     WPI; 2003-615964/58
                                        LABAT
                                                                                                           Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                       (LABA/)
(STAC/)
(DICK/)
(JONE/)
                           (DRMA/)
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The invention relates to an isolated polynucleotide comprising any one of 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is useful to generating antibodies specific for it. The present sequence for this patent did not form part of the printed specification, but was obtained in electronic format part of the printed specification, but was obtained in electronic format directly from USPFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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96.3%; Pred. No. 2.5e-53;
Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 22744; 44pp; English.
                                                                                                                                 30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                    30-JUL-2001; 2001US-00918995
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Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                             LABAT I.
STACHE-CRAIN B
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense DNA or RNA
                                                                                                                                                                                                                                                                      DRMANAC R T.
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US2003073623-A1.
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(DICK/) 1
(JONE/)
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RESULT 14

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-TGGCAGCCCAGCAAGCCCAGATAAGAAGACGTGCCCCATGAAGG
                                              374 AACGATATAGCCTTCAGCAGGAGAAGAACGATCCAGACAAGCCCAATTGCCACGCCAAGG
                                                                                               AAGGAAACCCCTTTGGCCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGC
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ABL13946/C
ID ABL13946 standard; cDNA; 3264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GCGATCCCAATGGCTACCTCACCTACTGTCCGTGTATGGGACGCTTTGGCAACCAGGCCG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 Accachrechedeareartedechredecaadecetraaredeaecerdarecredeced 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTGGCATACTGCTTTGAGG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from brosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 36323.
                                                                                                                                                                                                                        Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical, gene, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1209 BP; 302 A; 313 C; 307 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

15.1%; Score 166.4; DB 4; Length 12

Best Local Similarity 51.5%; Pred. No. 37e-37;

Matches 563; Conservative 0; Mismatches 486; Indels

Matches 563; Conservative 0; Mismatches 486; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                            ABL13947 standard; cDNA; 1209 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 GAGAAGCGGGTGGCATACTGCTTTGAGG------TGGCAGCCCCAGCGAAGC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGATAAGAAGACGTGCCCCATGAAGGAAGGAAACCCCTTTGGCCCATTCTGGGATCAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCATGTGAGTTTCAACAAGTCGGAGCTTTTTACAGGCATTTCCTTCAGTGCTTCCTAC 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), protessed DNA Sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 36320; 21pp + Sequence Listing; English.
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13.7%; Score 150.4; DB 4; Length 3
Best Local Similarity 50.9%; Pred. No. 2.4e-32;
Matches 541; Conservative 0; Mismatches 476; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
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                                                                                                                                                                                                                              23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
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1204 ATCAGTGTGCACAAGCTGCCGGAGGATGATCCTTACCTGGACTTGGCCATTCTCGGACAG 1145
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ATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAGGCCCAGATTCATGCCCACCTTGTC 624
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Search completed: November 9, 2005, 04:43:20 Job time : 644.158 secs THIS PAGE BLANK (USPTO)

355525 MA UI-E-EJO-UI-E-CL1-

BP459416 AUI37536

BP457865 AU117392 UI-M-HN0-601487689

CK36699 CR3689492 BCN348922 AU137536 BM711905 BM711905 BM711905 BM711905 BM711905 CN459072 CN459072 CN459072 CN459073 BES715757 BES715757 BES7030 BKS19639 BKS19639

601900828 601150556 602578756

7968 Full

AGENCOURT AGENCOURT

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Mus muscu

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                   mRNA linear HTC 21-JUL-2004 of T cells (Jurkat cell line)
                                                                                                                                                                                                                                                                                                                                                                                                               CR617950.1
HTC; CNSLT_cDNA.
HTC; CNSLT_cDNA.
HOmo sapiens (human)

Li, Metazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, Web.; Gruber, C.; Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGCCCGCGGGCTCCTGGGACCCGGCCGTTACCTGCTCTACTGCCCCTGCATGGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Pred. No. 5e-291;
0; Mismatches 2; Indels
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10-normalized"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                 CR617950 nRNA full-length cDNA clone CS0DJ008YF12 of T cCt 10-normalized of Homo sapiens (human).
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ008YF12"
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AU137536
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BK449172 BX449172
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1 ATGCCCGCGGGGCTCCTGGGA........CTGCGGGACGAGTTCTGATT 1100
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(c) 1993 - 2005 Compugen Ltd.
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Post-processing:

Database

Scoring table:

Searched:

Perfect score:

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eli, W.B., Gruber.C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Lupublished (2001)

On May 5, 2003 this sequence version replaced gi:30371746.

Contact: Ganoscope

Contact: Ganoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: sequence was primed with a Noti-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
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// organism="Homo sapiens"
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// db_xref="taxon:9606"
// db_xref="taxon:9606"
// dore="taxon:9606"
// db_xref="taxon:9606"
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                                                                                    mRNA linear EST 08-APR-2004
COT 25-NORMALIZED Homo sapiens
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BX353274 Homo sapiens NETROBLASTOWA COT 25-NORV
CDNA clone CSODC003YJII 5-PRIME, mRNA sequence.
BX53274
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92.8%; Pred. No. 8.9e-235;
tive 32; Mismatches 35;
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Group Phase I w II Team.

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Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs

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                                                 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suhi,Y., Ishii,Y., Nakamura,S., Hazama,M., Nishin-T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yongaya,Y., Inoue,Y., Miramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Please visit our web site for further details
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Mus musculus 10 days neonate cerebellum cDNA, RIKEN enriched library, clone:B930076G19 product:protein O-fucosyltransferase 1, full insert sequence.
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High-efficiency full-length cDNA cloning
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Db 1121 AGCGGGACCTCCATGGGAGGCAGTCGTCTTTGGCATGGACAGACCTCCCAGCTTC 1180 Qy 1085 GGGACGACTTCTGAT 1099 Db 1181 GGGATGAGTTTTGAT 1195	RESULT 4 AK044629 LOCUS LOCUS LOCUS Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930028F21 product:protein O-fucosyltransferase 1, full insert sequence. ACCESSION AK044629.1 GI:26336652 KEYWORDS HTC; CAP trapper. SOUNCE Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) REFERENCE Haysoria Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE Lannacia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. AUTHER High-efficiency full-length cDNA cloning MEDLINE 99279253 PUDRNED 10349636			AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase 1 & II Team. TITLE de0,70 ct the mouse transcriptome based on functional annotation of 60,70 ctull-length cDNAs JOURNAL Nature 420, 563-573 (2002) REFERENCE (bases 1 to 2616) AUTHORS Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Hashizume, W., Hayashida, K., Kurihara, C., Matsuyama, T., Kadawa, I., Kathoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kathoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kathoh, H., Kawai, J., Saltoh, H., Sakai, K., Ohno, M., Ohato, N., Okazaki, Y., Saitoh, R., Sakai, K., Sakazume, N., Sagabo, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., TITLE Direct Submission
Query Match B0.5%; Score 885.4; DB 3; Length 3611; Best Local Similarity 88.0%; Pred. No. 1.3e-232; Matches 964; Conservative 0; Mismatches 131; Qy 5 CGGCGGGCTCCTGGGATCCGGGTTACCTGTTACTGCTCTGCATGGGGGGCTTTG 64 Db 101 CAGCGGGCTCCTGGGACCTGGCCGGTTACCTGCTCTACTGCTCTGCTGCTGCATGGGGGCTTTG 160		365 GAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTGGGAGCTTT 461 GAAATCCTTTTGGCCATTCTGGGACCAGTTCATGTGAGTTTCAATAAGTCAGAACTGT 425 TTACAGGCATTTCCTTCAGTGCTTCCTACAGAACAATGGAGCCAGAGATTTCTCCAA 425 TTACAGGCATTTCCTTCAGTGCTTCCTACAGAACAATGGAGCCAGAGATTTCTCCAA 425 TTACAGGCATTTCCTTCAGCGCTCCTACAGAACAATGGACCCAGAGATTTCTTCGGAA 485 AGGAACATTCCTTCAGCGCTCCTACAAAGAACAATGGACCCAGGAATTTCTGCAA 486 AGGAACATTCCTTCAGCGCCTCCTACAAAGAACCCAGAGATTTCCTGCAA 487 AGGAACATTCCTTCAGCGCCCCCAGAGAACCCAGAGAACCAAGAAAACAAGAACCCAGAACACACAAGAAACAAAAAA	Db S81 AAGAGCATCCTGTGTTCTTGTTCTTCTTCTTTCTTGTAGTTCTTCTTCTTTCT	Db 821 CTCAGTGTGGGCTATAGCCGCACAGCGACCCTCTCACCATGACCATGTGCCTCC 880

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AGENCOURT 6611915 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5431669
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Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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CWGRFGWQADHFLGSLAPAKLLNRTLAVPPWIEYQHHKPPFTNLHVSYQKYFKLEPLQ
AYHRVVSLEDFWENLAPSHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQF
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
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O-fucosyltransferase 1 (MGD|MGI:2153207, GB|NM_080463,
evidence: BLASTN, 99%, match=1290)
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db_xref="faxon:10090"
/clone="A930028F21"
/tissue_type="retina"
/clone_lb="RIKEN full-length enr/dev_stage="adult"
34. .1215
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Pred. No. 2.6e-232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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964; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX345989 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED HOmo sapiens CODJO08YF12 5-PRIME, mRNA sequence. BX345989
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                                                                                                                                               GCCCAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTC 897
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1 (Dases 1 to 841)
1 in W B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                 898 TTCAAA--GGGAAGGTGAAGGTGGTG--AGCCTGAAGCCTGAGGTGGCCCAGGTCGACCT
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Pred. No. 1.1e-186;
1; Mismatches 2; Indels 1.
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGGCATTCATCTGCGCATTGGC 657
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Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1904 row: e column: 14
High quality sequence stop: 629.
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llarity 93.0%; Pred. No. 1.3e-193;
Conservative 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5431669"
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German Genome Project.

No s1 sequence available.
This clore (DKF2P76200115) is available at the RZPD in FPlease contact the RZPD: Ressourcenzentrum, Heubnerweg (Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
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Pred. No. 1.9e-186;
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larity 99.9%;
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1 (bases 1 to 719)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Conter (DKE2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCTGAGAAGCGGGTG
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                                                                                 ACCTTGGCTGTCCCTTCGCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC
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DKFZp76200115 5', mRNA sequence.
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequencepe.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                      CITITITACAGGCATITICCITCCTTCCTACAGAGAACAAIGGAGCCAGAGATITICI 566
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         420
                                               447 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 506
                                                                                                                                                                                                                              CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCAGTTCCCCGTCCTAGAA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687 GCCCAGATTCATGCCCCAGCTGGTCCGGCCACTATGTGGGGCATTCATCTGCGCATTGGCTC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCAGATTCATGCCCACCTTGTCCGGCC-CTATGTGGGCATTCATCTGCGCATTGGCTC 659
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31030014.
      361 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG
                                                                                                                CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT
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This sequence belongs to sequence cluster 9880.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOAM014AF066p1&c=9980.f.
Location/Qualifiers
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//organism="MINA"
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//lab host="Ditiols"
//lab host="Ditiols"
//ord="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
//ord="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
//ord="Organ: pooled lung and spleen; Library is oligo-dr spleen, and 20-22 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (ExoRv site is destroyed upon cloning). Average insert size is and directions and was constructed by C. Gruber fill-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                               BUKARYOCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; BUKARYOCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1. (bases 1 to 889)

S. NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Ingublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

http://image.llnl.gov account.

High quality sequence stop: 880.
81524031
603055202F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201616 5',
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                                                                                                             BI524031.1 GI:15348823
                                                                                                                                                                      Homo sapiens (human)
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Best Local Similarity 99.1
Matches 758; Conservative
                                                        mRNA sequence.
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         and Magness, C.L.
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/lab host="Electromax DH10B"
/lab host="Ratze MNLV"
/lone lib="Katze MNLV"
/note="Organ: Tiver; Vector: pDONR 222; Site_1: BsrG
Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                          Email: cmagness@illumigen.com
Sequenced on 2004.07.21. 611 Q20 bases. Library Preparation:
Michael Katze Lab at University of Washington DNA Sequencing:
Hilumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 942;
                                                                                  USA
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Large-Scale Rhesus Macaque cDNA Sequencing Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Best Local Similarity 94.1%; Pred. No. 3.3e-174;
Matches 743; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                            /organism="Macaca nemestrina"
/mol type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                   FORWARD: CCCTCACTAAAGGGGAACAAAA
BACKWARD: CACTATAGGGGGAATTGGGTA
INSERT Length: 942 Std Brror: 0.00
Plate: CL000531 row: E column: 09
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
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/clone="IBIUW:29960"
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                                                                                                                                                                                        http://www.macaque.org
pcr PRimers
                                                                                                               Fax: 2063780408
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Macaca nemestrina
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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ILLUMIGEN MCQ_51950 Katze_MNLV Macaca nemestrina cDNA clone
IBIUW:29960 5' similar to Bases 7 to 852 highly similar to human
POFUTI (Hs.178292), mRNA sequence.
CO774833. GI:50976096
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                                                                                                                                        TITIGGGAACCAGGCCGATCACTICTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAAACCGT
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                   Score 706.6; DB 5;
Pred. No. 2e-183;
4; Mismatches 10;
                 tch 64.2%;
al Similarity 97.8%;
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CCAAAGGAACATCCGGTGCTTGCCCTGCGGGAGCCCGGGCCCAGTT GAACACAGGCCACTACAGAAGTACATGGTATGGT	Oy 719 CCTCTCCGCAGTGTGGG-CTAAAGCGCAGCACAG-CGGCCCCCTCACGATGACTAT 776 Db 815 CCTCTCCCGAATGTGGGGGCCTACCCCAACAGCGCCCCCCTCCCGAAGCTAT 874 Oy 777 GTGCCTGCT 786 Db 875 GTGCCTGCCT 884 RESULT 11 BG747760 BG747760 BG747760 BG747760 BG747760 BG747760 BG747760 BG747760 BG7775255591 N1H_MGC_43 Homo sapiens CDNA Clone IMAGE:4842061 5',	ACCESSION BG747760 BG74760 BG747	Email: Tissue CDNA CDNA CDNA CDNA FOUND Hutpi- High c	/ (Jab host= "MRIMDB (phage-resistant)" / (Jone 11b="NIH MGC 42") / (Jone 11b="NIH MGC 42") / (Jone 11b="NIH MGC 42") / (Jone 12b="NIH MGC 42") / (Jone 12b="NIH MGC 42") / (Jone 12b="NIH MGC 41") / (J

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AGENCOURT 10055799 NIH MGC_134 Mus musculus cDNA clone
IMAGE:6509783 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 134"
/note="Vector: pCNV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
/note="Vector: pCNV-SPORT6.1; Site 1: Average insert size 1.7 kb. Constructed by Resden, Invitrogen Corp. Note: this is a NIH_MGC Library."
                                                                                                    721 AGGTGGTGAGTCTGAAACCTGAGGTGGCCCAGATCGACCTGTACATCCTTGGCCAGGCTG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov.
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14077 row: j column: 24
High quality Sequence Stop: 702.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 988)
                              TCGCCACGGACTCTGAGAGTTACCTGCGGAGATCCAGCAGCTCTTCAAAGGAAAGGTGA
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                                                                                   AGGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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87.3%; Pred. No. 9e-165;
ive 0; Mismatches 103; Indels
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/db_xref="taxon:10090"
/clone="IMAGE:6509783"
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National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Fax: +81-29-838-8627
Fax: +81-29-838-8627
Exail: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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/clone_lib="full-length enriched swine cDNA library, adult ovary"
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E 1 (bases 1 to 874)

I (bases 1 to 874)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Gaptos-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI757540 874 bp mRNA linear EST 25-SEP-2001 603029639F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199862 5', mRNA sequence.
BI757540 GI:15749118
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/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="thyAGE:5199862"
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/clone_lib="thy care anonymous pool of 6 male_brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoreN site e is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Courcement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 947)
11H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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larity 86.9%; Pred. No. 1.6e-162;
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166.4
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114.6
108.6
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42.4
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471.4
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Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 168, App
                                                                                                                        9, 2005, 08:00:04; Search time 984.698 Seconds (without alignments) 9238.165 Million cell updates/sec
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                                                                                                                                                                                                                                1100
1 ATGCCCGCGGGGCTCCTGGGA......CTGCGGGACGAGTTCTGATT 1100
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1: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*
5: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*
6: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*
7: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
8: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
10: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
11: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
11: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*
12: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*
13: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*
14: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*
15: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*
16: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*
17: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*
18: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*
19: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*
20: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*
21: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*
22: /cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq:*
23: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
24: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
25: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
26: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
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27: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
28: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
29: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
20: /cgn2 6
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-774-954-1
US-09-774-954-4
US-09-774-954-5
US-10-301-822-168
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
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seq length: 200000000
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Maximum DB
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Sequence 4752, Apple Sequence 9986, Apple Sequence 6032, Apple Sequence 4751, Apple Sequence 1034, Apple Sequence 1160, Apple Sequence 1160, Apple Sequence 136, Apple Sequence 1941, Apple Sequence 134, Apple Sequence 114, Apple Sequence 115, Apple Sequence 114, Apple Sequence 114, Apple Sequence 115, Apple Sequence 114, Appl
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Sequence 39272, A
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winhatin (Genentech)
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION DATA:
APPLICATION DATA:
RELING DATE: 26-NOV-1997
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
US-10-369-493-39272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
ITILE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
BDDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spellman
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CTGCCTGACCTGAAGGAGTCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
                           Gaps
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US-09-774-954-1
US-09-774-954

Sequence 1, Application US/09774954

Publication No. US20040241645A1

GENERAL INFORMATION:
MADER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE Genemitech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA

SOFTWARE: WINDER: WINDER: US/09/774,954

FILING DATE: 30-404

RELING DATE: 31-404

PILING DATE: 31-4097

ATTORNEY AREA INFORMATION:
MARK: SYODAGA, CTAIG G.

REGISTRATION NUMBER: US/08/978,741

PILING DATE: 31-30-404

REGISTRATION NUMBER: 1997

ATTORNEY AGRATION NUMBER: 39,044

REGISTRATION NUMBER: 91041P1

TELEROAM INCORMATION:
TELEROAM INCORMATI
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                 0;
                                               NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMUNICATION INTERER: P1041P1
TELEPAN: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CIRRACTERISTICS:
LENGTH: 1100 base pairs
TYPE: NUCleic Acid
STRANDEDNESS: Single
GSTRANDEDNESS: Single
GSTRANDENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
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QY 1081 CTGCGGGACGACTTCTGATT 1100	RESULT 3 US-09-774-954-4 ; Sequence 4, Application US/09774954 ; Publication No. US20040241645A1 ; GENERAL INFORMATION: APPLICANT: Yang Wang, Michael W. Spellman ; TITLE OF INVENTION: O-Fucosyltransferase	; NUMBER OF SEQUENCES: 17 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Genentech, Inc. ; STREET: 1 DNA Way ; CTTY: South San Francisco	STATE: California COUNTRY: USA ILLE: 94080	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS COPPUTER: Minney Minney Companies	CURRENT APPLICATION DATA: ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/774,954 ; FILING DATE: 30-Jan-2001	; CLASSIFICATION: <unknown> ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/08/978,741 ; FILING DATE: 26-NOV-1997</unknown>	APPLICATION NUMBER: 08/792,498 ; FILING DATE: 31-JAN-1997 ; ATTORNEY/ACENT INFORMATION: ; NAME: Svoboda, Craig G.	REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: P1041P1 TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1489	INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1300 base pairs	; TYPE: Nuclear Acid ; STRANDEDNESS: Single ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:	Ouery Match Best Local Similarity 99.9%; Score 1098.4; DB 11; Length 1300; Best Local Similarity 99.9%; Pred. No. 0; Matches 1099; Conservative 0; Mismarches 1: Indels 0: Gans 0:	1 ATCCCCCCCCCCCCCCCCCCCCCCCCCCTAACCTCCTCTAACCCCCC	61 TITGGGAACCAGGCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCTT 12 196 TITGGGAACCAGGCGATTCTTTGGGCTCTCTGGCATTTTGCAAAGCTGCTAAACCTT 12 196 TITGGGAACCAGGCGATTCTTTTTGGGCTTCTTTTTTTTTT	121 ACCTTGGCTGTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 18	Oy 181 CATGTGTGCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC 240	Oy 241 AGCTTGGAGARTTCANGGAGAAGCTGGCACCCACTGGCCCCTGAGAAGCGGGTG 300
1 ATGCCCGCGGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGCGC 60	61 TTTGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 120	181 CÀTGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATC 240 	241 AGCTTGGAGGATTCATGGAGAAGCTGGCACCCCACCCCTGGCCAGAGAAGCGGGTG 300 	301 GCATACTGCTTTGAGGTGGCAGCCAGCGAGCCCAGATAAGAAGACGTGCCCATGAAG 360 	361 GAAGGAAACCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGGG 420 	421 CTTTTTACAGGCATTTCCTTCGGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT 480 	481 CCAAAGGAACATCCGGTGCTTGCCCTGCGAGGCCCCAGCTCCCCGTCCTAGAA 540 	541 GAACACACCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAG 600 	601 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT 660	661 GACTGGAAGAACGCCTGTGCCATGCTGAAGACGGCACTGCAGGCTCGCACTTCATGGCC 720 	721 TCTCCGCAGTGTGGGCTACAGCCGCAGCACACCCCCCCCTCACGATGACTATGTGC 780	781 CTGCCTGACCTGAAGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTGGCTGGATGCC 840 	841 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900			1021 CGGGAGCGGGACTCCAGGGAGGCCGTCTTCTTCTTCGGCATGGACAGGCCCCCTAAG 1080

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GCATACTGCTTTGAGGTGGCAGCCCAGCAAGCCCCAGATAAGAAGACGTGCCCCATGAAG 360
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                                                               disk
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1MM FC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURENT APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/08/78,741
FILING DATE: 36-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SYODDAG, CARG G
RGGISTRATION NUMBER: 39,04
REFERENCE/DOCKET NUMBER: 91
REFERENCE/DOCKET NUMBER: 92
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEFON: 650/225-1891
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERICSINGS:
LENGTH: 11284 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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TOPOLGGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-774-954-5
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                                                                                                                                     GAAGGAAACCCITTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 420
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                                                                 CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCCAGAGATTTTCT 480
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Sequence 5, Application US/09774954
Publication No. US20040241645A1.
GENERAL INFORMATION:
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
TOCRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
CITY: South San Francisco
STREET: California
COUNTRY: USA
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Query Match 99.7%; Score 1096:8; DB 16; Length 5218; Best Local Similarity 99.8%; Pred. No. 0; Matches 1098; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Oy 1 AIGCCGCGGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCTGCATGGGGCGC 60	Qy 61 TITGGGAACCAGCCGATCACTICTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 120	Oy 121 ACCTTGGCTGCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 180 Db 239 ACCTTGGCTGTCCCTCGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 298	Qy 181 CATGTGTCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGTCATC 240 Db 299 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC 358	Qy 241 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACC	QY 301 GCATACTGCTTTGAGGTGGCCAGCCAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360 DD 419 GCATACTGCTTTGAGGTGGCAGCCCAGCGAGACCCAGATAAGAAGACGTGCCCCATGAAG 478	QY 361 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 420 DD 479 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCAAGTGAGTTTCAACAAGTCGGAG 538	Oy 421 CTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAACAATGGAGCCAGAGATTTCT 480	QY 481 CCAAAGGAACATCCGGTGCTTGCCTGCCAGGCCCCAGCCCAGTTCCCGTTCCTAGAA 540 DD 599 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGCCCAGCCCAGCCCAGTTCCCGTCTAGAG 658	QY 541 GAACACAGGCCACTACAGAAGTACATGGTCAGACGAAATGGTCAAGACGGAGAG 600 DD 659 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGAAGACGAAATGGTCAGAAGACGGAAGA 718	0y 601 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGGCATTCATCTGCGCATTGGCTCT 660	Oy 661 GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGC 720 Db 779 GACTGGAAGAAGACCTGTGCCATGCTGAAGGACGGGACTTCATGGCC 838	Qy 721 TCTCCGCAGTGTGTGGGCTACAGCCGCAGCAGCGCCCCCCTCACGATGACTATGTGC 780 Db 839 TCTCCGCAGTGTGTGGGCTACAGCCGCAGCACAGCGGCCCCCCTCACGATGACTATGTGC 898	QY 781 CTGCCTGAACCTGAAGAAATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840 DD 899 CTGCCTGACCTGAAGAGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 958	QY 841 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCTAC 900 DD 959 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCTTC 1018	OY 901 AAAGGGAAGGTGAAGCTGAAGCTGAAGCTGAAGCTCGAGGTCGACTCGACTTGTACATC 960	Oy 961 CTCGGCCAAGCCGACTTTATTGGCAACTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020
Qy 601 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT 600 L	Oy 661 GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC 720	OY 721 TCTCCGCAGTGTGGGCTACAGCCGCAGCAGCGCCCCCTCACGATGACTATGTGC 780	Oy 781 CTGCCTGACGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840	OY 841 CAGICGGICTACGITGCIACTGAITCCGAGAGTTAIGIGCCIGAGCICCAACAGGICTIT 900	OY 901 AAAGGGAAGGTGAAGGTGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 960 	Oy 961 CTCGGCCAAGCCGACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAG 1020	Oy 1021 CGGGAGCGGCCCTCCAGGGGAGCCGTCTTCTTCGCCATGGACACGCCCCCTAAG 1080	Qy 1081 CTGCGGGACGACTTCTGATT 1100 .	RESULT 5 US-10-301-822-168 . Seminare 168 Innlination HE/10301822	Fublication No. US20030148410A1 GENERAL INFORMATION: APPLICANT: Millennium Pharmaceuticals, Inc.	APPLICANT: Guillemette, Tracy L. APPLICANT: Kamatkar, Shubhangi , APPLICANT: Schlegel, Robert , APPLICANT: Monahan John E	; APPLICANT: Thibodeau, Stephen N. ; APPLICANT: Burgart, Lawrence J. ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND ; TITLE OF INVENTION: METHODS FOR THEMSTORY ASSESSMENT DESIGNMENT AND	THICK, ROODSONENT, PREVENTION,	FRIOR FILING DATE: 2001-12-10 ; PRIOR FILING DATE: 2001-12-10 ; PRIOR APPLICATION NUMBER: US 60/361,978	FRIOR FILING DATE: 2022-03-03-03-03-03-03-03-03-03-03-03-03-03-	; SEQ ID NO 168 ; LENGTH: 5218 ; TYPE: DNA ; ORGANISM: Homo Saniens	

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RESULT 9
US-10-956-157-4751
; Sequence 4751, Application US/10956157
                                                                                   GGACGAGTICTGATT 1100
                                                                                              1021 GGACGAGTTCTGATT 1035
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milarity 99.8%; U
Conservative 0;
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Best Local Similarity
Matches 472; Conserv
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; ORGANISM: Homo
US-10-956-157-9986
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                                                                                                                 Gaps
                                                                                        Query Match 93.9%; Score 1033.4; DB 11; Length 5009; Best Local Similarity 99.9%; Pred. No. 4.1e-314; Matches 1034; Conservative 0; Mismatches 1; Indels 0;
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       SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
LENGTH: 5009 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID IUS-09-774-954-7
INFORMATION FOR SEQ ID NO: 7:
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RESULT 8

US-10-956-157-9986

US-10-956-157-9986

US-10-956-157-9986

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: WPWER

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: US00 (AM 10.001)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NO 9986
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CCAAGCCGACCATTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGA
                                                                            GCGGGACCTCCAGGGGAGGCCGTCTTCTTTCGGCATGGACAGGCCCCCTAAGCTGCG
                                                                                                          GCGGGACCTCCAGGGGGGCGTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCG
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Pred. No. 1.9e-137;
0; Mismatches 1;
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                                                                                    656 GCTCTGACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCA
                                                                                                                                                                  TGGCCTCTCCGCAGTGTGGGCTACAGCCGCAGCACAGCGGCCCCCTCACGATGACTA
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    Length 10331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-918-95-19437
Sequence 19477, Application US/09918995
Publication No. US20030073623A1
General Information:
TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TILLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TILLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TILLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TILLE OF INVENTION: 100 PS 09/918, 995
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILLING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARRE: FRAESEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 19937
      Score 251.2; DB 10; Length
Pred. No. 9.4e-68;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTCAAAGGAAAGGTATGTGTGG 2743
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US-09-18-955-22744
US-09-18-955-22744
F. Sequence 22744, Application US/09918995
F. Publication No. US20030073623A1
GENERAL INFORMATION:
FAPLICANT: Hyseq, Inc.
         Match 22.8%;
Local Similarity 97.0%;
Les 256; Conservative (
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ORGANISM: Homo sapiens
US-09-918-995-19437
           Query Match
Best Local S:
Matches 256
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Publication No. US20050118625A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: WILLiam
TITLE OF INVENTION: HUMAN OSTEOARTHAITIS AND HUMAN PROTEASES
FILE REFERENCE: 03.1996-04.3000 (AM 10.1081)
CURRENT APPLICANTON: WHOSER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATCHIN Version 3.2
SEQ ID NO 4751
LENGTH: 1506
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                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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CITITIACAGGATTICCTICAGTGCTICCTACAGAAACAATGGAGCCAGAG 591
CITITIACAGGATTICCTICAGAGAAAAAAATGAAGGCAGAG 591
                                                                                                                                                                                                                                                                                                                                                    Score 471.4; DB 22; Length 1506;
Pred. No. 1.9e-137;
0; Mismatches 1; Indels 0;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6032
LENGTH: 10331
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PCOO
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.8%;
Matches 472; Conservative
                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4751
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; ORGANISM: Homo sapiens
US-09-764-891-6032
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US-09-764-891-6032
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Gaps

199 196 253 256

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ATCACTICITIGGCCICTCTGGCATITIGCAAAGCTGCTAAACCGTACCTTGGCTGTCCCTC 136
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                                                                                                                                                                                                                                                            Length 1209
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                                                                                                                                                                                                                                                            DB 26;
                                                                                                                                                                                                                                                      15.1%; Score 166.4; DB 26; 51.5%; Pred. No. 2.4e-41; tive 0; Mismatches 486;
            NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 18161
LENGTH: 1209
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.5'
Matches 563; Conservative
                                                                                                                                   TYPE: DNA ORGANISM: DROSOPHILA
                                                                                                                                                                        ; ORGANISM: DROSO:
US-11-097-143-18161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 221.8; DB 10; Length 477;
Pred. No. 5.9e-59;
0; Mismatches 8; Indels 1;
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EXPRESSION OF 10,000
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC.
TITLE OF INVENTION: DRAGAS, FOR DETECTING EXPI
TITLE OF INVENTION: DRAGAS, FOR DETECTING EXPI
TITLE OF INVENTION: DRAGAS.
FILE REFERENCE: CLOOD'28
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 06/157,832
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR PRILOR TOWNERS: 60/175,693
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
                                              CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILIAND DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PSECSEQ for Windows Version 3.0
LENGTH: 477
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Publication No. US20050208558A1
GENERAL INFORMATION:
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R FILING DATE: 2000-01-12
R APPLICATION NUMBER: 60/184,831
RR FILING DATE: 2000-02-24
RR APPLICATION NUMBER: 60/191,637
RR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
20.2%;
Best Local Similarity 96.3%;
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(477)
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RESULT 15
US-09-783-590-11501
US-09-783-590-11501
Sequence 11501, Application US/09783590
Sequence 11501, Application US/09783590
Sequence 11501, Application US/09783590
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haddong
APPLICANT: Rosen, Craig A.
APPLICANT: Roben, Craig A.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 1995-04-12
FRIOR FILING DATE: 1995-04-12
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                                                                                                                                                               ccagacaagcccaarraccacgccaaggarggcaarccrrrriggrccrrrriggacacr 1745
                                                                                                                                                                                                                                                                                                                                                                             1684 AGCAACGAGGCTGCCAÁGTGGCAGACCAATATCCTGCAGAATCATATCCCGTACTCGCG 1625
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                                                     1864 rcégagicagigicatrificiacaagaaacararagcerrcagcagagaagar 1805
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                                                                                                                CCAGATAAGAAGACGTGCCCCATGAAGGAAGGAAACCCCTTTGGCCCATTCTGGGATCAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 ATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAGCCCCAGATTCATGCCCACCTTGTC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 GTGGGCTACAGCCGCACACAGCGCCCCCTCACGATGACTATGTGCTGCTGCTGACCTG 792
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                                                                                                                                                                                                                                                                      TITCACATAGACTITGTGCGGTCAGAGTTCTATGCGCCACTTCATTTTGATGTGCATCAT
                                                                                                                                                                                                                                                                                                                              AG-----AGAACAATGGAGCCAGAGATTTTCTCCAAAGGAACATCCGGTGCTTGCC
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      289 GAGAAGCGGGTGGCATACTGCTTTGAGG-
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US-11-097-143-18160/C

Sequence 18160, Application US/11097143

Publication No. US20050208558A1

GENERAL INFORMATION:

APPLICANT: 0 = 1

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION CONTRACT, SOS, 04-04

FRIOR APPLICATION NUMBER: 60/157, 832

PRIOR APPLICATION NUMBER: 60/160, 191

PRIOR APPLICATION NUMBER: 60/160, 191

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-110-19

PRIOR PILING DATE: 1999-110-19

PRIOR PILING DATE: 2090-00-12

PRIOR APPLICATION NUMBER: 60/173, 383

PRIOR PILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: 60/173, 383

PRIOR APPLICATION NUMBER: 60/173, 383

PRIOR PILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: 60/173, 831

PRIOR PILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: 60/173, 831

PRIOR APPLICATION NUMBER: 60/173, 831

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEQ. ID NOS: 43008

SOSTWWARE: PASSENCE OF WINDOWN VERSION 4.0

LENGTH . 2084
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                                                                                                                                                                                              CCTCCTTCACTGCCTTTGTGAAGGGGGAGCGGGACCTCCAGGGGAGGCCGTCTTTCT 1057
                                                                                                                                      1034 ATCCTTACCTGGACTTGGCCATTCTCGGACAGTCGAACCACTTTATCGGCAACTGTATAT 1093
                                                                                                                                                                                                                                             1094 cererracerdedarredaaaaaaddaacdadargaddedacdedarrecarcererrer 1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 CTGCTAAACCGTACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCGGGTCATCAGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACTGGCCCCCT 288
                                                                                    --- CCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCTTTATTGGCAACTGTGTCT
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                                                                                                                                                                                                                                                                                                     1058 TCGGCATGGACAGG 1071
                                                                                                                                                                                                                                                                                                                                                          1154 GGGGATTCCCCAAG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OKGANISM: DROSO!
US-11-097-143-18160
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178 CTCCATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 Arcadcrirggadgarrircargaaaaacragcacccaccacragacccurrgagaagc 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 10.4%; Score 114.6; DB 9; Length 402;
Best Local Similarity 83.9%; Pred. No. 3.4e-25;
Matches 177; Conservative 0; Mismatches 23; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 CGTGCCCCATGAAGGAAGGAAACCCCTTTGG 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: 1(22)

OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (46)

OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (272)
OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (301)
OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (302)
OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (333)
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LOCATION: (342)
OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (374)
OTHER INFORMATION: n equals a,t,g, or c, LOCATION: (386)
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LOCATION: (386)
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LOCATION: (386)
OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc feature
LOCATION: (390)
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LOCATION: (390)
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LOCATION: (390)
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LOCATION: (390)
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (22)
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11501
LENGTH: 402
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Search completed: November 9, 2005, 15:51:17 Job time : 988.698 secs

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Patent No. 5386025 Patent No. 5386025

Sequence 1,

Sequence 191, Sequence 221,

Sequence Sequence

Sequence 1 Sequence Sequence

Sequence 11943, R Sequence 12011, R Sequence 11977, R Sequence 13025, R Sequence 1, Appli

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Run on:

Sequence:

Searched:

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ATGCCGCGGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGGCGC
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US-09-940-3168-1

US-09-252-991A-11943

US-09-252-991A-11977

US-09-252-991A-11977

US-09-252-991A-11977

US-09-949-016-13025

US-08-016-13025

US-08-014-0838-1

US-08-314-0838-1

US-08-314-0838-1

US-08-314-598-1

US-08-315-551-21

US-10-237-551-221

US-09-294-2988-24
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Sequence 16, Application US/08978741

Patent No. 61007076

Patent No. 61007076

APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: 0-Fucosyltransferase NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: 1 DNA Way

CITY: South San Francisco

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: 3.5 inch, 1.44 Mb floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1100;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAME: Syoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET UMBER: P1(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 1100; Conservative
                                                   1650
102053
1843
5962
5962
5975
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STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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                                                                                                   9, 2005, 02:15:54 ; Search time 199.044 Seconds (without alignments) 9042.764 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                     US-09-774-954-16
1100
1 ATGCCCGCGGGCTCCTGGGA.......CTGCGGGACGAGTTCTGATT 1100
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Sequence 1,
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Sequence 16, Application US/0933729A
Sequence 16, Application US/0933729A
Patent No. 6270997
APPLICANT: Mang/Yaba
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: 0-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US/09/33, 729A
CURRENT FILING DATE: 1999-06-15
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 1100
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ORGANISM: Homo Sapien
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ATGCCGGGGGCTCCTGGGACCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC ATGCCCGCGGGGGCCCGGCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC ATGCCCGCGGGGCCCGGGCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC ATGCCGGGGCCGGTTACCTGGCTCTACTGCGCTCTAGGGGCGC ATTGGGGAACCGGTCTTCTTGGGGTTTTGCAAAGCTGCTAAACGT ATGGGAACCAGGCCGATCATTCTTGGGATTTGCAAAGCTGCTAAACGT ATGGGAACCAGGCCCTTTGGATTGAGTACCAGCATCACAAGCTCCTTTCACCAACCTC ATGCCTTGGCTTGCTTGGATTGAATTGAATTGAATTGAA	181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATGGGTCATC		361 GAAGGAAACCCCTTTGGCCC 	421 CTTTTTACAGGGATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT 4	481 CCAAAGGAACATCCGGTGCT 	541 GAACACGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGA 6	601 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGCTCT 6	661 GACTGGAAGGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC 7	721 TCTCCGCAGTGTGTGGGCTACAGCCGCACACAGCGGCCCCCCTCACGATGACTATGTGC 7	781 CTGCCTGACCTGAAGGAGTCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 8	841 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATC	901 AAAGGGAAGGTGAAGGTGACCTGAAGCCTGAGGTGGCCCAGGTCGACGTGTACATC 9	961 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1	1021 CGGGAGCGGGACCTCCAGGGAGCCGTCTTCTTCTTCGGCATGGACAGGCCCCCTAAG 1
TGCC 840	960 1020 1020	GCCCCCTAAG 1080	TGCGGGACGAGTTCTGATT 1100	US-08-978-741-1 ; Sequence 1, Application US/08978741 ; Patent V 06-010076 ; GRNTRA1, INFORMATION.	APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: D	ADDRESSEE: Generatech, Inc. ; STREET: 1 DNA Way ; CITY: South San Francisco ; California	COUNTRY: USA ZIP: 94080 COMPUTER REALANBLE FORM: DD	COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible COMPUTER: MINPERIN (PC-DOS/MS-DOS SOFTWARE: WinPerin (Genentech) COMPUTER: MINPERIN (Annual DAME) COMPUTER:	CONTAIN AFELICATION NUMBER: US/08/978,74	APPLICATION DAIR: FILING DATE: 31 ATTORNEY/AGENT INFORMATION: MANAGE CONSTRUCTOR DESCRIPTION: DAILORNEY/AGENT INFORMATION: DAILORNEY/AGENT INFORMATION:	* * * * *	TELEPHONE: 650/525-1489 TELEPHONE: 650/592-9881 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: DD	Nucleic Acid Nucleic Acid Nucleic Single Y: Linear	Os.00-3/0-/41-1 Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1021 CGGGAGCGGGACCTCCCAGGGGAGGCCGTCTTCTTTCGGCATGGACAGGCCCCCTAAG 1080
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                                                                                             TCTCCGCAGTGTGTGGGGCTACAGCCGCACAGCGGCCCCCCTCACGATGACTATGTGC
                                                                                                                                                               GACTGGAAGAACGCCTGTGCCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
                                                                     TCTCCGCAGTGTGGGGCTACAGCCGCAGCACAGCGGCCCCCCTCACGATGACTATGTGC
                                                                                                                                           CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGGATGCTCGCTGGATGCC
                                                                                                                                                                                                                 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCCTGAGGCTCCAACAGCTCTTC
   GACTGGAAGGACCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1489
TELEPHONE: 650/252-1489
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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US-08-978-741-4

| Sequence 4, Application US/08978741
| Patent No. 6100076
| GENERAL INFORMATION:
| TITLE OF INVENTION: O-FUCOSYLITANSFERSES
| TORRESPONDENCE ADDRESS:
| ADDRESSES Genentech, Inc.
| STREET: 1 DNA WAY
| CITY: South San Francisco
| STATE: California
| COUNTRY: USA
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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100.0%; Score 1100; DB 3; Length 1514;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                         APPLICANT: Wang Yang
APPLICANT: Wang Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Phocosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
SEQ ID NO 2
RESULT 4
US-09-333-729A-2
'S Sequence 2, Application US/09333729A
'Patent No. 6270987
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFRENCE: Pl041PlD1-Subsetitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT APPLICATION NUMBER: US 08/798,741
PRIOR PILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
99.9%; Score 1098.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 0; Mismatches
                                                                           CTGCGGGACGAGTTCTGATT 1100
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US-09-333-729A-6
Sequence 6, Application US/09333729A
Patent No. 6770987
GENERAL INFORMATION:
APPLICANT: Wang Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Plasmid insert.
US-09-333-729A-6
                                                                                              CTGCGGGACGAGTTCTGATT
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                              1156
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Best Local Similarity
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                                                                                                                                                                                                           99.9%; Score 1098.4;
99.9%; Pred. No. 0;
live 0; Mismatches
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11284 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Matches 1099; Conservative
                                                                                                                                           Linear
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                                                                                                 GCCCAGATTCATGCCCACTTGTCCGGCCCTATGTGGGGCATTCATCTGCGCATTGGCTCT
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                                                                     GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCCATTCATCTGCGCATTGGCTCT
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
COMPUTER
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Patent No. 610076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCGGGACGAGTTCTGATT 1100
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Db 121 GTCCTACCAGAAGTACTTCAAGCTGGAGCCČCTCCAGGCTTACCATCGGGTCATCAGCTT Oy 246 GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCTGAGAAGCGGGTGGCATA	181	Qy 306 CTGCTTTGAGGTGGCAGCCCAGCAGAGAGAGAGAGAGGAGAGGAGAGGAGGA	Qy 366 AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGAGTTTCAACAAGTCCGAGCTTTTTTTT	301 426 361	486	Qy 546 CAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGAGAGGCCCA	Qy 606 GATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGACTG	Qy 666 GAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACGCTCTCC	Oy 726 GCAGTGTGTACAGCCGCAGCACAGCGGCCCCCCTCACGATGACTATGTGCCTGCC	QY 786 TGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTC	Qy 846 GGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGG	QY 906 GAAGGTGAAGCTGAAGCCTGAAGCTCAGGTGGCCCAGGTCGACCTGTACATCCTCGG DD	QY 966 CCAAGCCGACCACTTTATTGGCAACTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGA DD 901 CCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGA	Oy 1026 GCGGGACCTCCAGGGAGGCCGTCTTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCG	Oy 1086 GGACGAGTTCTGATT 1100 	RESULT 9 US-09-333-729A-8 ; Sequence 8, Application US/09333729A ; Patent No. 62709B7 ; GENERAL INPORMATION: ; APPLICANT: Wang, Yang ; TILE OF INVENTION: ; FILE REFERENCE: P1041P1D1-Substitute
901 AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCTGAGGTGGCCCAGGTCGACCTGTACATC 960 [CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG	5196 CTCGGCCAACCATTTATTGGCAACTGTGTCTCCTTCATTGACTGCTTTTTTTT			REGULT 8 US-08-398-741-7 Sequence 7, Application US/08978741 ; Patent No. 6100076	GENERAL INFORMATION: APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17	CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco	STAIE: CALIFORNIA COUNTRY: USA ZIP: 94080 COMPUTER READABLE FORM:	MEDIUM TYPE: 3.5 INCh, 1.44 MD LIOPPY GISK COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)	CORKENI APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 610076-1997 CLASSIFICATION: 435	FALCATICATION DATA: APPLICATION NUMBER: 08/792498 FILING DATE: 31 ATTORNEY/AGENT INFORMATION:	NAME: SVODGOG, CYAIG G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: P1041P1 TELECOMMUNICATION INFORMATION:	Inlerpure: 650/252-984 TELEPAX: 650/952-984 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:	LENGHI SOUD BASE DAIRS TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear Lengh Stranded Strand	Ouery Match 93.9%; Score 1033.4; DB 3; Length 5009; Cuery Match Similarity 99.9%; Pred. No. 8.3e-302; Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	66 GAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTT 125

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15.3%; Score 168; DB 4; Length 1320;
Best Local Similarity 51.6%; Pred. No. 2.9e-40;
Matches 564; Conservative 0; Mismatches 485; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA; ORGANISM: Drosophila melanogaster
US-09-270-767-14353
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                                                                                                                                 Length 5009;
                                                                                                                                                         Indels
                                                                                                                               DB 3;
                                                                                                                               Ouery Match 93.9%; Score 1033.4; DB 3 Best Local Similarity 99.9%; Pred. No. 8.3e-302; Matches 1034; Conservative 0; Mismatches 1.
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 8
                                                                                          Homo Sapien
                                                                                             ; ORGANISM: HOU
US-09-333-729A-8
                                                                LENGTH: 500
TYPE: DNA
ORGANISM: 1
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28905
                                           TCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTCGGTCTACGTTGCTA
                                                                                                            288 CCATTAAGAACGTGCGCCAAACTCAGCCGGACAACGAAATCAAATCAGTTTTCGTGGCGT
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Pred. No. 3.2e-07;
0; Mismatches 64
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; Sequence 28905, Application US/09270767
; Patent No. 6703491
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ORGANISM: Drosophila melanogaster
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Best Local Similarity
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LENGTH: 2034
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30507
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US-09-270-767-30507
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; LENGTH: 19228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16285
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Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PRILIG DATE: 2000-04-14

PRIOR APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16285
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US-09-949-016-12127/C
| Sequence 12127, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION: PAPPLICATION: PAPPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REPERENCE: CLOO1307
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REPERENCE: CLOO1307
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,756
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NOS: 207012
| PRIOR PILING DATE: 2000-09-08
| SOFTWARE: FastSEQ for Windows Version 4.0
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                                                        Query Match 5.3%; Score 58.6; DB 4; Length 2034; Best Local Similarity 60.2%; Pred. No. 4.8e-07; Matches 97; Conservative 0; Mismatches 64; Indels 0;
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5.1%; Score 56; DB 4; Length 19227;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 56; Conservative 0; Mismatches 0; Indels
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US-09-949-016-16285/c
US-09-270-767-13022
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; ORGANISM: Human
US-09-949-016-12127
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